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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:44:58 2000; MasPar time 5.30 Seconds 205.769 Million cell updates/sec

ar output not generated.

Description: Perfect Score: >US-09-290-049-2 (1-20) from US09290049.pep 135 1 VPSYSFIRTAHDSEVQDLIA 20

Scoring table: PAM 150 Gap 15 Sequence:

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb19
1:sp_archea 2:sp_bacteria 3:sp_fung1 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 28.249; Variance 35.475; scale 0.796

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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STREPTOCOCCUS MUTANS. BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; STREPTOCOCCUS.	01-AUG-1998 (TREMBLREL. 07, CREATED) 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) GLUCOSYLTRANSFERASE-SI.	LT 2 O69388 PRELIMINARY; PRT; 1455 AA.	1 VPSYSFIRTAHDSEVQDLI 19	- 1	Query Match 82.2%; Score 111; DB 2; Length 1390; Best Local Similarity 94.7%; Pred. No. 2.83e-12; Matches 18; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	SEQUENCE 1390 AA; 155375 MW; C211E7B8 CRC32;	D88655; D1027046	FEMS MICROBIOL. LETT: 161:331-336(1998).	"MOLECULAR analyses of glucosyltransferase genes among strains of	S.;	FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA S., OOSHIMA T., SOBUE S.,		SEQUENCE FROM N.A.	[1]	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;	STREPTOCOCCUS MUTANS.	GLUCUSYLIKANSFERASE-SI. GTFC.	. 08, LAST ANNOTATIO	07,	TREMBIRET.	O69385 PRELIMINARY; PRT; 1390 AA.	1

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MEDLINE; 98231643.
FUJUWARA T., TERAO Y
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069382;
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069397
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"Molecular analyses of glucosyltransferase
Streptococus mutans.";
FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D88652; D1027042; -.
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"Molecular analyses of glucosyltransferase
Streptococus mutans.";
FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D88658; D1027050; -.
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01-AUG-1998 (TREMBLREL.
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GLUCOSYLTRANSFERASE-SI.
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GLUCOSYLTRANSFERASE-SI.
 MEDLINE; 98231643.
FUJIWARA T., TERAO Y.,
KIMURA S., HAMADA S.;
"Molecular analyses of
                                           SEQUENCE FROM N.A. STRAIN-MT4467;
                                                                                     STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
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FUJIWARA T., TERAO Y., HOSHINO T.,
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AC 069391;
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DT 01-NOW-1998 (TREMBLREL. 0)
DT 01-OV-1998 (TREMBLREL. 0)
DE GLUCOSYLTRANSFERASE-SI.
GN GTFC.
OS STREPTOCOCCUS MUTANS.
OC BACTERIA; FIRMICUTES; BAC.
OC STREPTOCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MT4251;
RX MEDLINE; 98231643.
RA FUJUWARA T., TERAO Y., HO:
RA KIMURA S., HAMADA S.;
RT "MOLECULAR analyses of gl.
RT Streptococcus mutans.";
RI Streptococcus mutans.";
RI FEMS MICROBIOL. LETT. 161
DR EMBL; D88661; D1027044;
SQ SEQUENCE 1455 AA; 1628
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MEDLINE; 98231643.
FUJIWARA T., TERAO Y.,
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FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D89978; D1027060; -.
TRANSFERASE.
SEQUENCE 1455 AA; 162914 MW; 7D729DA
                                                                                                     "Molecular analyses of glucosyltransferase Streptococcus mutans."; FEMS MICROBIOL. LETT. 161:331-336(1998).
                                                                                                                                                                                                                                                                                                           BACTERIA; FIRE STREPTOCOCCUS.
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STRAIN=MT4239;
MEDLINE; 98231643.

A FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA S.
A KIMURA S., HAWADA S.;
T "Molecular analyses of glucosyltransferase general streptococcus mutans.";
FEMS MICROBIOL. LETT., 161:331-336(1998).
                                                                                                                                                                                                                                                                                                                                                                              Query Match 82.2%;
Best Local Similarity 94.7%;
Matches 18; Conservative
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FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA S., FUJIWAR S., HAMADA S.;
"Molecular analyses of glucosyltransferase gestreptococcus mutans.";
"TYPE MICROBIOL. LETT. 161:331-336(1998).
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STREPTOCOCCUS.
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EMBL; D88657; D1027049;
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18; Conservative
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STREPTOCOCCUS MUTANS.
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FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D89977; D1027059; -.
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FEMS MICROBIOL. LETT. 161:331-336(1998).
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"Molecular analyses of glucosyltransferase
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FUJIWARA T., TERAO Y.,
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FUJIWARA T., TERAO Y.,
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Molecular analyses of glucosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D13858; D1003482; -...
PFAM; PF00128; alpha-amylase; 1.
SIGNAL; TRANSFERASE; GLYCOSYLTRAN
SIGNAL
1 38 POTI
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SATO S., INOUE M., HANDA N., AIZAWA Y., I
SATO S., INOUE M., HANDA N., AIZAWA Y., I
SATO S., INOUE M., HANDA N., AIZAWA Y., I
SATO S., INOUE M., HANDA N., AIZAWA Y., I
SATO S., INOUE M., INOUE M.,
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ANN. KAGOSHIMA UNIV. DENTAL SCHOOL 16:23-29(1996).
EMBL; D63570; D1010438; -.
PEAM; PF00128; alpha-amylase; 1.
                                                                                                                     01-JUN-1998 (TREMBLREL. 06, CREATED)
01-JUN-1998 (TREMBLREL. 06, LAST SEQUENCE UPDATE)
01-JUN-1998 (TREMBLREL. 06, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE (EC 2.4.1.5) (DEXTRANSUCRASE)
CSUCROSE 6-GLUCOSYLTRANSFERASE).
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Q59983
                               LEUCONOSTOC MESENTERO BACTERIA; FIRMICUTES;
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01-NOV-1996 (TREMBLREL 01, LAST
01-JAN-1999 (TREMBLREL 09, LAST
GLUCOSYLTRANSFERASE-I PRECURSOR
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STREPTOCOCCUS SOBRINUS.
BACTERIA; FIRMICUTES; E
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16; Conser
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                  MESENTEROIDES.
IRMICUTES; BACTILUS/CLOSTRIDIUM GROUP; LACTOBACILLACEAE;
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llarity 84.2%;
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TOSOR (EC 2.4.1.5) (DEXTRANSUCRASE) (SUCROSE)
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GLUCOSYL)(N+1).
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X MEDLINE; 95122197.

X MEDLINE; 95122197.

The STATESON C.L., GIFFARD P.M., JACQUI STATESON ATCC 25;

The STATESON C.L., GIFFARD P.M., JACQUI STATESON ATCC 25;

Coding for primer independent gluce infect. IMMUN. 63:609-621(1995).

EMBL; L35495; G662379; -.

PFAM; PF00128; alpha-amvlacc.
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Q1-NOV-1996
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Q48756;
Q48756;
01-NOV-1996
01-NOV-1996
01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MONCHOIS V., WILLEMOT R.M., REMAUD-SIMEON M., CROUX C., MONSAN P.; "Cloning and sequencing of a gene coding for a novel dextransucrass from Leuconostoc mesenteroides NRRL B-1299 synthesizing only alpha (1-6) and alpha (1-3) linkages."; GENE 182:23-32(1996).
EMBL; U38181; G1022963; -.
EFAM; PF00128; alpha-amylase; 1.
SEQUENCE 1290 AA; 145590 MW; F4460B13 CRC32;
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SIGUENCE FROM N.A.
STRAIN-WRRL B-1299;
MONCHOIS V., REMAUD-SIMEON M., MONSAN P., W
PEMS MICROBIOL. LETT. 0:0-0(1998)
-1- CATALYTIC ACTIVITY: SUCROSE +
-(1.6-ALPHA-D-GLUCOSYL)(N) - D-FRUCTOSE
(1.6-ALPHA-D-GLUCOSYL)(N+1).
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LEUCONOSTOC MESENTEROIDES.
BACTERIA; FIRMICUTES; BACI
                                                                                                                                                                                                                                                                                     GLUCOSYLTRANSFERASE GTFL.
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STRAIN-NRRL B1299;
MEDLINE; 97136686.
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TRANSFERASE; GLYCOSYLTRANSFERASE.
SEQUENCE 1508 AA; 168511 MW;
                                                                                                                                                                                                                                       STREPTOCOCCUS SALIVARIUS.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM
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15; Conservative
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14; Conservative
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(TREMBLREL.
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(TREMBLREL. 08, LAST ANNOTATION
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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78.9%;
                                                                                                                                                                                                                                                                                                            PRECURSOR
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                                                                                    glucosyltransferases
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KW SIGNAL; TRANSFERASE.

FT SIGNAL 1 35 1449 GLUCOSYLTRANSFERASE.

FT CHAIN 36 1449 GLUCOSYLTRANSFERASE.

SO SEQUENCE 1449 AA; 159984 MW; E9A4BA87 CRC32;

Query Match 60.0%; Score 81; DB 2; Length 1449;

Best Local Similarity 55.0%; Pred. No. 8.67e-05;

Matches 11; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Matches 11; Conservative 7; Mismatches 1; Indels 1; Gaps 1;

Db 607 MANYAFVR-AHDSEVQSIIG 625

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Qy 1 VPSYSFIRTAHDSEVQDLIA 20

Search completed: Tue Jan 11 15:45:45 2000

Job time: 47 secs.
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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:47:50 2000; MasPar time 2.45 Seconds 254.053 Million cell updates/sec

ar output not generated.

Description: Perfect Score: Sequence: >US-09-290-049(3)
(1-22) from USB9290049.pep
155
1 TGARTINGQLLYFRANGVQVKG 22

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 29.681; Variance 38.978; scale 0.761

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	o	U	4	ω	2	1	esult No.
61	62	62	62	63	63	63	63	63	63	63	65	65	67	70	72	79	93	104	106	112	114	155	Score
39.4	40.0	40.0	40.0	40.6	•	40.6	40.6	40.6	40.6	•	41.9		43.2		46.5	51.0	60.0	67.1	68.4	72.3	73.5	100.0	Query Match
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	1.95e+00		1.95e+00	1.27e+00	٠	1.27e+00	1.27e+00		1.27e+00	1.27e+00	5.32e-01	5.32e-01	2.19e-01	5.58e-02	2.20e-02	7.50e-04	5.53e-07	1.36e-09	. 46e	1.49e-11	4.74e-12	9.19e-23	Pred. No.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
58	58	58	58	58	59	59	59	59	59	59	59	60	60	60	60	60	60	60	61	61	61
37.4	37.4	37.4	37.4	37.4	38.1	38.1	38.1	38.1	38.1	38.1	38.1	38.7	38.7	38.7	38.7	38.7	38.7	38.7	39.4	39.4	39.4
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ASSOCI	KINASE	ZINC P	INTEGRIN BETA-7 SUBUNI	HYPOTHETICAL 29.9 KD P	PENTAFUNCTIONAL AROM P	TYPE-A		EPHRIN TYPE-A RECEPTOR	PROTEIN	HYPOTHETICAL 35.2 KD P	HYPOTHETICAL 30.7 KD P	TRANSCRIPTION FACTOR S	TRANSCRIPTION FACTOR S	HYPOTHETICAL PROTEIN T	CANNABINOID RECEPTOR 1	-	CANNABINOID RECEPTOR 1	CANNABINOID RECEPTOR 1	LACTICIN 481/LACTOCOCC	MURAMA	HYPOTHETICAL 44.6 KD P
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FROR	88888888	ននននន	8888888	CCCCRRRRRRR	RESULT AC P AC P DT 0 DT 0 DT 1 DE G GN G G
EMBL; M17361; G153640; PIR; B33135; B33135. PFAM; PFOUL28; alpha-amylase; 1. TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES. SIGNAL 1 34 POTENTIAL.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	GLUCANS: - I SUMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-BINDING PROTEIN FROM S.MUTANS.	-!- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) - D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL) (N+1)!- SUBCELLULAR LOCATION: SECRETED!- DISEASE: DENTAL CARIES!- GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN-GS-5; MEDLINE; 87308013. SHIROZA T., UEDA S., KURAMITSU H.K.; SHIROZA T., UEDA S., KURAMITSU H.K.; "SEQUENCE analysis of the 9tfB gene from Streptococcus mutans."; 1. BACTERIOL. 169:4263-4270/1982). - I- FUNCTION: PRODUCTION OF EXTERACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS	GTFB_STRMU STANDARD; PRT; 1475 AA. 6TFB_STRMU STANDARD; PRT; 1475 AA. 908987; 01-NOV-1988 (REL. 09, CREATED) 01-NOV-1988 (REL. 37, LAST ANNOTATION UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE) (SUCROSE 6-GLUCOSYLTRANSFERASE). GTFB. STREPPOCOCCUS MUTANS. BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCCACEAE; STREPPOCOCCUS.

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Best Local
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01-JUL-1989
15-DEC-1998
CHAIN
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                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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sobrinus MFe28.";
J. BACTERTOT
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                                                                                                               TRANSFERASE;
SIGNAL
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FERRETTI J.J., GII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1-JUL-1989 (REL. 11, CREATED)
1-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
5-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
LUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
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11001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: SECRETED.
DISEASE: DENTAL CARIES.
DISEASE: DENTAL CARIES.
GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCONS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAN OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND BINDING PROTEIN FROM S.MUTANS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 155; DB 1;
Pred. No. 9.19e-23;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RUSSELL R.R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
A REPEAT.
A TANDEM REPEATS.
                   CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
1.25 A, 2 B, AND 5 AC REPEATS
                                                                                       GLUCOSYLTRANSFERASE-I
                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4542C1D6 CRC32;
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B
                                                                                                                                       REPEAT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GTF-I) (DEXTRANSUCRASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene from Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOME TO A GLUCAN.
                                                                                                                                       DENTAL CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Best Local S
Matches 1
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P27470;
01-AUG-1992
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                                                                                                                               PIR; A38175; A38175.
PFAM; PF00128; alpha-amylase; 1.
HSSP; P00695; 2HEE.
                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
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STREPTOCOCCUS DOWNEI (STREPTOCOCCUS SOBRINUS)
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (REL. 23, CREATED)
01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 91123227.
ABO H., MATSUMURA T.,
                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREPTOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                             TRANSFERASE;
                                                                                                                                                                                                 EMBL; D90213; G217033; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. BACTERIOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAU OF THEIR ABILITY TO ADHERE TO SMOOTH SUFFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISEASE: DENTAL CARIES.
GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBI GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: SECRETED.
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17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED SE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE
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                                                                                                           GLYCOSYLTRANSFERASE;
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77.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
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Pred. No. 4
GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BLUDING (APPROXIMATE).
6.5 X TANDEM REPEATS.
                                                                                        POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                           SIGNAL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₽
                                                                                                             REPEAT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              AND SOME TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1597;
                                                                                                             DENTAL CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                              A GLUCAN-
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glucan
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                                                                                                                                                                                                                                                                                                                                                       outstation
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P13470; P05427;
01-NOV-1988 (REL. 09, CREATED)
01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4.1.5) (GT
(DEXTRANSUCRASE) (SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                 SHIROZA T., UEDA S., KURAMITSU H.K.;

"Sequence analysis of the gtfB gene from Streptococcus mutans.";

J. BACTERIOL. 169:4263-4270(1987).

-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAL
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-i- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) =
D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL) (N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTFC_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
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REPEAT
                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send in a massit to its removed.
                                                                                                                                                                                                                                                             <del>+ +</del>
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REPEAT
                        EMBL; M22054; G153643; -.
EMBL; M17361; G153641; -.
PIR; JT0345; JT0345.
PIR; C33135; C33135.
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 87308013.
SHIROZA T., UEDA S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
PFAM; PF00128; alpha-amylase; 1. TRANSFERASE; GLYCOSYLTRANSFERASE;
                                                                                       or send
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-349 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 89137980.
UEDA S., SHIROZA T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence analysis of ENE 69:101-109(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 77.3%;
hes 17; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ب
                                                                                                                                                                                                                                                          DISEASE: DENTAL CARIES. GTF-I SYNTHESIZES WATER
                                                                                                                                                                                                                                GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
                                                                                                                                                                                             SIMILARITY: TO OTHER BINDING PROTEIN FROM
                                                                                                                                                                                                                        GLUCANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGARTINGQLLYFRANGVQVKG
              PF00128;
                                                                                        an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KURAMITSU
f the gtfC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176167
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                                                                                                                                                                                           GLUCOSYLTRANSFERASES AND S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1319
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Pred. No. 1.49e-11;
2; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H.K.;
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273A23FA CR
 SIGNAL; REPEAT; DENTAL CARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from Streptococcus mutans GS-5.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC32;
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                                                                                                                                                                                                         SOME TO A GLUCAN-
                                                                                                                                                       a collaboration
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                                                                                                                                                                                                                                                                                                                       GILMORE K.S., RUSSELL R.R., FERRETTI J.J.;

"Analysis of the Streptococcus downei gtfs gene, which specifies a glucosyltransferase that synthesizes soluble glucans.";

INFECT. IMMUN. 58:2452-2458(1990).

-i- FUNCTION: PRODUCTION OF EXTRACELULIAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-DEC-1992 (REL. 24, CREATED)
01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-ARR-1993 (REL. 25, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE'S PRECURSOR (EC 2.4.1.5)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
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SEQUENCE
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                                                                                                                                                           the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
                                                                                                                                                                                                                                                                          -i- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
-i- ENZYME REGULATION: GLUCAN SYNTHESIS BY GTF-S IS INDEPENDENT PRIMER GLUCAN UNLIKE GTF-I.
                                                                                                    EMBL; M30943; G1536
PIR; A41483; A41483
                                                                                                                                   entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREPTOCOCCUS DOWNEI (STREPTOCOCCUS SOBRINUS).
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P29336;
01-DEC-1992
                                                                     SIGNAL
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                                                                                TRANSFERASE;
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                                                                                                                                                                                                                             GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                  DISEASE: DENTAL CARIES
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GLYCOSYLTRANSFERASE;
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2.4 A, 1 C AND 1 AC REPEATS.

A REPEAT.

C REPEAT.

C REPEAT.
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A REPEAT ()
MW; 3EA372
OR 37 (POTENTIAL).
GLUCOSITRANSTERASE-S.
GATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMP
4.5 X TANDEM REPEATS.
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Pred. No. 4.46e-10;
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                                                                              SIGNAL;
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                                                                                                                                                                      There are no rest
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                                                                            REPEAT; DENTAL CARIES.
                                 (APPROXIMATE)
                                                                                                                                                           Usage
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SEQUENCE
1332 TGSQTIAGKKLYFASDGKQVKG
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
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                                                                                                                                   DOMAIN
REPEAT
                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                       SEQUENCE
                                                                                                                                                                            TRANSFERASE; GLYCÓSYLTRÁNSFERASE; SIGNAL; REPEAT; DENTAL SIGNAL 1 ? POTENTIAL.
                                                                                                                                                                                                                                                   entitles requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence of the Streptococcus mutans gtfD gene encoding the glucosyltransferase-S enzyme.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
                                                                                                                     REPEAT
                                                                                                                                                                                                                       EMBL; M29296; G153645; -
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FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOMENT OF THE DENTAL PLAQUE BECAN
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) -
D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY:
BINDING PROT
                                                                                                                                                                                                                                                                                                                                                                                                      GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF GLUCANS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DISEASE: DENTAL CARIES
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                                            Similarity
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                                                                                       1430
                                                                                                                                                                                                                                                                                                                                                                       ITY: TO OTHER GLUCOSYLTRANSFERASES PROTEIN FROM S.MUTANS.
                             Conservative
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Pred. No. 1.36e-09;
5; Mismatches 3;
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3 X 63 AA APPROXIMATE TANDEM REPEATS
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RESULT 7
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DT 01-FEB-1996 (REL. 3
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RT SEQUENCE FROM N.A.
RC STRAIN-S288C / FY16
RX MEDLINE; 96408711.
RA KATSOULOU C., TZERM
RT 1-CHOMOSOME XI "SEQUENCE AND STRAIN-S288C / FY16
RT 1-CHOMOSOME XI "SEQUENCE AND STRAIN-S288C / TERM
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MEDLINE; 94016561.
LEHNHERR H. MAGUIN E. JAFRI S.,
"Plasmid addiction genes of bacter
death on curing of prophage, and p
prophage is retained.";
J. MOL. BIOL. 233:414-428(1993).
-i- FUNCTION: KILLS CELLS. DOC AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1995
01-NOV-1995
01-NOV-1995
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Q06259;
                 LOSS.

THE CONCENTRATION OF PHD IN P1 LYSOGENS IS FAR GREATER THAN OF THE POISON IT ANTAGONIZES. SUCH AN EXCESS MAY ASSUME THE WELL-BEING OF CARRIERS OF THE ADDICTING PLASMID.
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KATSOULOU C., TZERMIA M., TAVERNARAKIS N., ALEXANDRAKI D.;
"Sequence analysis of a 40.7 kb segment from the left arm of chromosome X reveals 14 known genes and 13 new open reading including homologues of genes clustered on the right arm of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL PROTEIN. SEQUENCE 382 AA; 4
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EMBL; X87371; G854550; -.
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EUKARYOTA; FUNGI; ASCOMYCOTA; HEMIASCOMYCETES;
                                                                                                                                                                                                                                                                                                                                                                                               BACTERIOPHAGE P1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            DEATH ON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                     VIRUSES; DSDNA VIRUSES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YEAST 12:787-797(1996).
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                                                                                                                         STABILIZE PLASMID
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(REL. 32, LAST SEQ
(REL. 32, LAST ANN
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(REL. 33, LAST SEQUENCE UPDATE)
(REL. 33, LAST ANOTATION UPDATE)
(44.9 KD PROTEIN IN INO1-IDS2 INTERGENIC
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32, LAST ANNOTATION UPDATE)
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                                                                                                                         NUMBER
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Pred. No.
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7.50e-04;
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                                                                                                                       PROTEIN FUNCTION IN NG A LETHAL RESPONSE
                                                                                                                                                                                                                     prevents
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doc, which
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Best Local
                                                                               P16154;
01-APR-1990
01-FEB-1996
01-NOV-1997
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01.010358;
01.NOV-1997 (REL. 35, CREATED)
01.NOV-1997 (REL. 35, LAST SEQUENCE UPDATE)
01.NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
HYPOTHETICAL 59.0 KD PROTEIN PRECURSOR (ORF119).
ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMNPV).
VIRUSES; DEDNA VIRUSES, NO RNA STAGE; BACULOVIRIDAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
     CLOSTRIDIUM DIFFICILE
                                                           TOXIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; VIROLOGY 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M95666; G463277; -. PIR; S38555; S38555.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AHRENS C.H., RUSSELL R.R., ROHRMANN G.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 97271300.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                               (REL. 14, CREATED)
(REL. 33, LAST SEQ
(REL. 35, LAST ANN
                                                                                                                                                                                                                                                                                                                                                                                                             45.2%;
llarity 42.9%;
Conservative
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58983 MW;
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ANNOTATION UPDAT
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7; 1
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Pred. No. 5.58e-02
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HYPOTHETICAL PROTEIN ORF119.
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CLOSTRIDIUM.
[1]
                                                                                                                                                                                                                                                                        PTER_MOUSE STANDARD; PRT; 349 AA. 060866; 050866; 15-DEC-1998 (REL. 37, CREATED) 15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) PHOSPHOTRIESTERASE RELATED PROTEIN (PARATHION
                       SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-KIDNEY;
MEDLINE; 96194889.
HOU X., MASER R.L., MAGENHEIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X51797; G40441; -. EMBL; M30307; G144926; -. EMBL; X92982; E212010; -. PIR; S08638; S08638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VPI 10463;

VON EICHEL-STREIBER C.;

VON EICHEL-STREIBER C.;

SUBMITTED (JAN-1997) TO EMBL/GENBANK/DDBJ DATA BANKS.

-I- DOMAIN: THE C-TERMINAL PART OF TOXIN A CONSISTS OF A 833

REPETITIVE STRUCTURE. THIS PART OF TOXIN A IS COMPOSED OF DIFFERENT OLIGOPEPTIDES.

-I- DISEASE: CLOSTRIDIUM DIFFICILE PRODUCES TWO TOXINS, AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 90129305.
DOVE C.H., WANG S.Z., PRICE WILKINS T.W., JOHNSON J.L.;
                                                                                                                                                                                 MUS MUSCULUS (MOUSE).
EUKARYOTA; METAZOA; C
                                                                                                                                                                                                                                                        PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2460 TGLRTIDGKKYYFNTNTAVAVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. STRAIN-VPI 10463;
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                                                                                                                                                            RODENTIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular characterization of the Clostridium difficile toxin A
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Similarity 52.2%;
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     L., MAGENHEIMER B.S., and liver-expressed
                                                                                                                                                      CHORDATA; VERTEBRATA; THI; MURIDAE; MURINAE;
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3; 1
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Pred. No. 2.19e-01;
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                                                                                                                                                      MAMMALIA; EUTHERIA;
MUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2710;
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GENE 168:157-163(1996).
-i- COFACTOR: CONTAINS 2 MOLES OF ZINC PER SUBUNIT (BY SIMILARITY).
-i- TISSUE SPECIFICITY: EXPRESSED IN KIDNEY AND LIVER.
-i- SIMILARITY: BELONGS TO THE PHOSPHOTRIESTERASE FAMILY.
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                KALIMAN A.V., KRYUKOV V.M., BAYEV A.A.; "The nucleotide sequence of bacteriophage between early and late genes."; NUCLEIC ACIDS RES. 16:6230-6230(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 95309401.
KALIMAN A.V., KULSHIN V.E.,
KRYUKOV V.M.;
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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VIRUSES; DSDNA VIRUSES,
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abnormal expression in injured and polycystic kidneys.";
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Best Local :
Matches
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P24721;
01-MAR-1992 (REL. 21, CREATED)
01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                     *Mouse asialoglycoprotein receptor cDNA sequence: conservation of receptor genes during mammalian evolution.";

BIOCHIM. BIOPHYS. ACTA 1087:259-261(1990).

-I- EUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX CARBOHYDRATE MOIETIES HAS BEEN REMOVED. THE RECEPTOR RECOGNIZES TERMINAL GALACTOSE AND N-ACETYLGALACTOSAMINE UNITS. AFTER LIGAND BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE DISASSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
                                                                                                                                                        PIR;
                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL. the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MUS MUSCULIS (MOUSE).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
EUKARYOTA; METAZOA; CHORDATA; WORIDAE; MURINAE; MUS.
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PROSITE; PS00615; C_TYPE_LECTIN_1;
PROSITE; PS50041; C_TYPE_LECTIN_2;
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                                                                DOMAIN
                                                                            CALCIUM;
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S01982; S01982.
PROTEIN.
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                                                                             GLYCOPROTEIN; RECEPTOR; ENDOCYTOSIS; SIGNAL-ANCHOR; PHOSPHORYLATION.
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1396 AA;
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O59128;
15-DEC-1998 (REL. 37, CREATED)
15-DEC-1998 (REL. 37, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
14-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
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YAMAMOTO S., SEKINE M., BABA S., KOSUGI H.,
SAKAI M., OGURA K., OTSUKA R., NAKAZAWA H.,
FUNAHASHI T., TANAKA T., KUDOH Y., YAMAZAKI
AOKI K., KIKUCHI H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete sequence and gene organization of the genome of a thermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA RES. 5:55-76(1998).
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"Molecular cloning and expression pattern of rpr-1,
resiniferatoxin-binding, phosphotriesterase-related
expressed in rat kidney tubules.";
FEBS LETT. 410:378-382(1997).
                                                                                                                                                                                                                                                                                                                                         -i- FUNCTION: BINDS REŠINIFÉROTOXIN, A VANILLOID THAT DESENSITISES NOCICEPTIVE NEURONS.
-i- COFACTOR: CONTAINS 2 MOLES OF ZINC PER SUBUNIT (BY SIMILARITY)
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Description: (1-22) from US09290049.pep
Perfect Score: 155

Sequence: 1 TGARTINGQLLYFRANGVQVKG 22

Scoring table: PAM 150 Gap 15

Searched: 179066 segs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: sptremb19

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Statistics: Mean 29.020; Variance 39.036; scale 0.743

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA KIMURA S., HAMADA S.;

"Molecular analyses of glucosyltransferase Streptococcus mutans.";

FEMS MICROBIOL. LETT. 161:331-336(1998).

EMBL: D88651; D1027041; -
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MEDLINE; 98231643.
FUJIWARA T., TERAO Y., HOSHINO T.,
KIMURA S., HAMADA S.;
"Molecular analyses of glucosyltran
                                                                                                                  SEQUENCE FROM N.A. STRAIN-MT4239;
                                                                                                                                                                                                                                 STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
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FUJIWARA T., TERAO Y.,
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SEQUENCE FROM N.A.
                                                                                                                                                                                                         STREPTOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-MT8148;
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21; Conser
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Similarity 95.5%;
21; Conservative
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(TREMBLREL.)
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   glucosyltransferase
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Pred. No. 5.35e-19;
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LAST SEQUENCE UPDATE)
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Pred. No. 5.35e-19
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                                                      OOSHIMA T.,
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RESULT 5
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DT 01-AUG-1998 (TREMBLREL 0)
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DT 01-OV-1998 (TREMBLREL 0)
DE GLUCOSYLTRANSFERASE-I.
GN GTFB.
OS STREPTOCOCCUS MUTANS.
OC BACTERTA; FIRNICUTES; BACCOCCUS.
RN [1]
RP SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
FUJIWARA T., TERAO Y., HO;
RA KIMURA S., HAMADA S.;
RT "MOLECULAR MANADA S.;
RT Streptococcus mutans.";
RL FEMS MICROBIOL LETT. 161
DR EMBL; D88660; D1027053; -
KW TRANSFERASE.
SQ SEQUENCE 1476 AA; 1658
                                            AC CONTRACTOR OF THE PROPERTY 
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FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D88657; D1027049; -.
TRANSFERASE.
                                                                                                                      "Molecular analyses of glucosyltransferase Streptococcus mutans.";
                                                                                                                                                                                                                                                                                                             STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
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                                                                                                     FEMS MICROBIOL.
                                                                                                                                                                 FUJIWARA T., TERAO Y.,
KIMURA S., HAMADA S.;
                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-MT4239;
                                                               TRANSFERASE
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                                                                                                                                                                                                       MEDLINE; 98231643
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larity 95.5%;
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                                                                                                                                                                                    HOSHINO
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LAST ANNOTATION UPDAT
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Pred. No. 5.
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No. 5.35e-19;
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FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA S., KIMURA S., HAMADA S.;

"MOLECULAR analyses of glucosyltransferase ge"

"Streptococcus mutans.";

"TEPTOCROBIOL. LETT. 161:331-336(1998).
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Best Local Similarity
Matches 16; Conser
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Best Local
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Matches
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STRAIN-MT4467;

MEDLINE; 98231643.

FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA S., O

KIMURA S., HAMADA S.;

"MOlecular analyses of glucosyltransferase genes

Streptococcus mutans.";

SEMBL, D89978; D1027060; -.
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01-AUG-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
GLUCOSYLTRANSFERASE-SI.
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                                      TGARVVNGQRLYFKSNGVQAKG 1350
TGARTINGQLLYFRANGVQVKG
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                                                                           Score 121; DB 2;
Pred. No. 2.28e-13;
3; Mismatches 3
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Pred. No. 2.28e-13;
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                                                                                                                                                                                                                                                                                                            KAWABATA S.,
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069391;
01-AUG-1998 (TREMBLREL. 0
01-AUG-1998 (TREMBLREL. C
01-NOV-1998 (TREMBLREL. C
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Q59983;
Q1-NOV-1996
Q1-NOV-1996
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SEQUENCE
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                                         1296 TGAQTIRGQXLYFKANGQQVKG 1317
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D13858; D1003482; -. PFAM; PF00128; alpha-amylase;
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"DNA sequence of the glucosyltransferase
streptococcus sobrinus.";
DNA SEQ. 4:19-27(1993).
-!- CATALYTIC ACTIVITY: SUCROSE + (1,6-AI
D-FRUCTOSE + (1,6-ALPHA-D- GLUCOSYL)(
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01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-JAN-1999 (TREMBLREL. 09, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (DEXTRANSUCRASE) (SUCROSE
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FUJTWARA T., TERAO Y., HOSHINO T., KAWABATA S., C
KIMURA S., HAMADA S.;
"MOLECULar analyses of glucosyltransferase genes
Streptococcus mutans.";
FEMS MICROBIOL LETT. 161:331-336(1998).
EMBL; D8866; D1027054; -.
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1590 AA; 175955 MW;
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LPHA-D- GLUCOSYL)(N+1).
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Pred. No. 7.
4; Mismatc
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Pred. No. 3.
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GLUCOSYLTRANSFERASE-I.
MW; FE6A57D7 CRC32;
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7.18e-13;
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e gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q55263
Q55263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            **GIFFARD P.M., SIMPSON C.L., MILWARD C.P., JACQUES N.A.;

**MOLECULAR Characterization of a cluster of at least two
glucosyltransferase genes in Streptococcus salivarius ATCC 25975.";

J. GEN. MICROBIOL. 137:2577-2593(1991).

-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOMENT OF THE DENTAL PLAQUE
BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE
THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-i- CAPALYTIC ACTIVITY: SUCROSE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q00600 PRELIMINARY; PRT; 1518 AA.
Q00600;
Q1-NOV-1996 (TREMBLREL. 01, CREATED)
Q1-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
Q1-NOV-1998 (TREMBLEEL. 08, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE I (EC 2.4.1.5) (GTF) (DEXTRANSUCRASE)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1383 TGAQVINGQHLYFNADGSQVKG 1404
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REPEAT
REPEAT
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REPEAT
                                                                                                                                    ANN. KAGOSHIMA UNIV. DENTAL SCHOOL EMBL; D63570; D1010438; -. PFAM; PF00128; alpha-amylase; 1.
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GIFFARD P.M., SIMPSON C.
                                                                                              TRANSFERASE.
SEQUENCE 1
                                                                                                                                                                                                               SATO S.;
                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-ATCC 33478;
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SUBCELLULAR LOCATION: EXTRACELLULAR.
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M64111; G153649; -.
PF00128; alpha-amylase;
    Similarity
15; Conser
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FIRMICUTES; BACILLUS/CLOSTRIDIUM
                                                                                           1590 AA;
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larity 72.7%;
Conservative
  70.3%;
larity 68.2%;
Conservative
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Score 109; DB 2; Le
Pred. No. 2.05e-10;
3; Mismatches 4;
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LAST SEQUENCE UPDATE)
LAST ANNOTATION UPDATE)
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Pred. No. 2.05e-10;
2; Mismatches 4
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PEPEAT 1.
PEPEAT 2.
PEPEAT 3.
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PEPEAT 5.
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                                                                                           47186F6A CRC32;
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                                           Length 1590;
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Indels
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RESULT 14

ID 69385;

AC 069385;

DT 01-AUG-1998

DT 01-AVU-1998

DE GLUCOSYLTRANG
GN GTFC.

OS STREPTOCOCCU

OC STREPTOCOCCU

OC STREPTOCOCCU

RN [1]

RP SEQUENCE FROM
RC STRAIN-WT424:

RX MEDLINE: 982:

RA KIMURA S., H

RT MOlecular an
RT MOLECULAR
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RL FEMS MICROBIC

RL TRANSFERARS.

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SQ SEQUENCE 1.
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ID 048756;
AC 048756;
DT 01-NOV-1996
DT 01-NOV-1998
DE DEXTRANSUCRAN
OS LEUCONOSTOC.
CHEUCONOSTOC.
RN [1]
RP SEQUENCE FROM
RT STRAIN-NRRL 1
RX MEDLINE; 971:
RA MONCHOIS V.
RT "Cloning and from Leuconos
RT (1-6) and all
RL GENE 182:23:
RL EMBL; U38181
DR EMBL; P500181
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Best Local Similarity 63.6%;
Matches 14; Conservative
                                                        Matches
                                                                   Query Match
Best Local
                                                                                                                    "Molecular analyses of glucosyltransferase streptococcus mutans.";
FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D88655; D1027046;
FRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEXTRANSUCRASE.
LEUCONOSTOC MESENTEROIDES.
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; LACTOBACILLACEAE;
                1264 TGTVTFNGQRLYFKPNGVQAKG
                                                                                                                                                                                                                                                                                                                                          01-AUG-1998 (TREMBLREL.
01-AUG-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
GLUCOSYLTRANSFERASE-SI.
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PFAM; PF00128; alpha-amylase; 
SEQUENCE 1290 AA; 145590 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 97136686.

MONCHOIS V., WILLEMOT R.M., REMAUD-SIMEON M., CROUX C., Cloning and sequencing of a gene coding for a novel dex from Leuconostoc mesenteroides NRRL B-1299 synthesizing (1-6) and alpha (1-3) linkages.";

GENE 182:33-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1410 TGEQTINGQHLYFKEDGHQVKG
|| :|||| ||| :|| |||
1 TGARTINGQLLYFRANGVQVKG
                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN-MT4245; MEDLINE; 98231643.
                                                                                                                                                                                                                                                                                     BACTERIA; FIRM
STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                                               STREPTOCOCCUS MUTANS
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STRAIN-NRRL B1299;
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1 TGARTINGQLLYFRANGVQVKG
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                                                        Similarity
15; Conser
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                                                                                                                1390 AA;
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                                                      68.4%;
larity 68.2%;
Conservative
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                                                                                                                                                                                                              TERAO Y., HOSHINO T., KAWABATA S.,
                                                                                                                155375
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08,
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MW;
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                                                                  Score 106;
Pred. No. 1.
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LAST ANNOTATION UPDATE)
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Pred. No. 6.24e-10;
3; Mismatches 5
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gene coding for a novel dextransucrase
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                                                        Mismatches
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RESULT 15

PRELIMINARY;

PRT;

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Search completed: Tue Jan 11 15:49:06 2000 Job time : 52 secs.
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SIMILAR
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-!- SUBCELULAR LOCATION: EXTRACELLULAR.
-!- DISEASE: DENTAL CARIES.
-!- SIMILARITY: TO REGIONS OF BARLEY AND BACILLUS AMYLOLIQUEFACIENS
-!- SIMILARITY: TO REGIONS OF BARLEY AND BACILLUS AMYLOLIQUEFACIENS
ALPHA AMYLASES AND RABBIT GLYCOGEN PHOSPHORYLASE.
EMBL; 211872; G47531; -
EMBL; 211873; G47528; -
EMBL; 211873; G47528; -
EMBL; M64111; G153650; -
EMBL; M64111; G153650; -
EMBL; M6410128; alpha-amylase; 1.
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MEDLINE; 92148377.
MEDLINE; 92148377.
MILWARD C.P., JACQUES N.A.;
"Molecular characterization of a cluster of at least two
glucosyltransferase genes in Streptococcus salivarius ATCC 25975.";
J. GEN. MICROBIOL. 137:2577-2593(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GIFFARD P.M., ALLEN D.M., MILWARD C.P., SIMPSON C.L., JACQUES N.A.; "Sequence of the gtfk gene of Streptococcus salivarius ATCC 25975 and evolution of the gtf genes of oral streptococci."; J. GEN. MICROBIOL. 139:1511-1522(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TREMBLREL. 01, CREATED)
01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)
01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE S PRECURSOR (EC 2.4.1.5) (GTF) (DEXTRANSUCRASE)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                     1402 TGAQVINGQHLYFDANGRQVKG 1423
                                                                                                                                                                                                          SEQUENCE
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q00599;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREPTOCOCCUS.
                                                                                                                                                                                                                                                                                        [RANSFERASE;
                                                                                                                                   y Match 68.4%; Score 106; DB 2; Local Similarity 77.3%; Pred. No. 1.09e-09; hes 17; Conservative 1; Mismatches 4
                                                                 1 TGARTINGOLLYFRANGVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE +

(1.6-ALPHA-D-GLUCOSYL)(N) - D-FRUCTOSE +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93381463
                                                                                                                                                                                                        43
867
1132
1599
                                                                                                                                                                                                                                                                                          GLYCOSYLTRANSFERASE;
                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                        1219
                                                                                                                                                                                                                                          1599
967
                                                                                                                                                                                                       99 GLUCOSYLTRANSFERASE S.
67 TO ALPHA-AMYLASES.
19 TO GLYCOGEN PHOSPHORYLASE.
176480 MW; 575C79C9 CRC32;
                                                                 22
                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                        SIGNAL; REPEAT; DENTAL CARIES.
                                                                                                                                     4; Indels
                                                                                                                                                                     Length 1599;
                                                                                                                                   0
                                                                                                                                   Gaps
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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Tue Jan 11 15:37:52 2000; MasPar time 5.64 Seconds 203.291 Million cell updates/sec

ar output not generated.

Description: Perfect Score: Sequence: >US-09-290-049-1 (1-21) from US09290049.pep 148 1 ANDHLSILEAWSDNDTPYT.HD 21

Scoring table: PAM 150 Gap 15

Searched: 179066 seqs, 54579741 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

sptremb19

1:sp_archea 2:sp_bacteria 3:sp_fungi 4:sp_human
5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
9:sp_phage 10:sp_plant 11:sp_rodent 12:sp_unclassified
13:sp_vertebrate 14:sp_virus

Statistics: Mean 28.660; Variance 41.580; scale 0.689

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Query Match	Lе	BB	Ħ	Description	Pred. No.
1	148	100.0	1390	ູລຸ	069385	GLUCOSYLTRANSFERASE-SI	8.69e-19
2	148	100.0	1455	N	069391	GLUCOSYLTRANSFERASE-SI	œ
w	148	100.0	1476	N	069390	GLUCOSYLTRANSFERASE-I.	8
4	148	100.0	1476	N	069381	GLUCOSYLTRANSFERASE-I.	
u	148	100.0	1476	ν	069384	GLUCOSYLTRANSFERASE-I.	
σ	148	100.0	1476	N	069396	GLUCOSYLTRANSFERASE-I.	
7	148	100.0	1476	N	069387	GLUCOSYLTRANSFERASE-I.	
œ	136	91.9	1455	Ŋ	069397	GLUCOSYLTRANSFERASE-SI	7.
9	136	91.9	1455	N	069388	GLUCOSYLTRANSFERASE-SI	7
10	136	91.9	1455	Ŋ	069382	GLUCOSYLTRANSFERASE-SI	7.09e-
11	131	88.5	1590	N	Q55263	GLUCOSYLTRANSFERASE GT	
12	131	88.5	1590	N	Q59983	GLUCOSYLTRANSFERASE-I	1.11e-14
13	101	68.2	1462	ν	069398	GLUCOSYLTRANSFERASE-S.	8.76e-08
14	101	68.2	1462	Ŋ	069386	GLUCOSYLTRANSFERASE-S.	8.76e-08
13	101	68.2	1462	N	069389	GLUCOSYLTRANSFEREASE-S	
16	101	68.2	1462	N	069392	GLUCOSYLTRANSFERASE-S.	8.76e-08
17	101	68.2	1462	N	069383	GLUCOSYLTRANSFERASE-S.	.
18	101	68.2	1508	Ŋ	052224	GLUCOSYLTRANSFERASE (E	80
19	95	64.2	1577	N	Q54178	GLUCOSYLTRANSFERASE.	1.78e-06
20	86	58.1	1449	N	Q55264	GLUCOSYLTRANSFERASE PR	
						-	

45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21
62	62	62	62	62	63	63	63	64	64	64	65	66	66	67	67	8	68	70	70	72	75	78	83	86
41.9	41.9	41.9	41.9	41.9	42.6	42.6	42.6	43.2	43.2	43.2	43.9	44.6	44.6	45.3	45.3	45.9	45.9	47.3	47.3	48.6	50.7	52.7	56.1	58.1
1009	602				403			594			581			525					549					1449
υı	1	13	14	Ŋ	10	14	14	14	5	10	N	N	10	ω	N	14	14	N	10	N	N	N	N	N
017380	Q63485	Q90893	Q85633	045983	023222	056851	056850	091465	P93344	023614	034023	007944	004073	059679	006579	P89062	P89063	005566	Q43274	084087	00600	Q00599	Q55265	068542
	RAT ACTIVATED C-RAF ON	C-MIL PROTO-ONCOGENE (V-MIL PROTEIN.	ZC513.10 PROTEIN.	MADS-BOX PROTEIN HOMOL	NSP4.	NSP4.	CHITINASE.	ALDEHYDE DEHYDROGENASE	PSII D1 PROTEIN PROCES	HYPOTHETICAL 66.2 KD P	S	О	HYPOTHETICAL 60.3 KD P	HYPOTHETICAL 52.0 KD P	NSP4.	NSP4.	PPDK.	T CYTOPLASM MALE STERI	HYPOTHETICAL 65.4 KD P	GLUCOSYLTRANSFERASE I	GLUCOSYLTRANSFERASE S	GLUCOSYLTRANSFERASE PR	GLUCOSYLTRANSFERASE N
5.59e+00	5.59e+00	5.59e+00	5.59e+00	5.59e+00	3.75e+00	3.75e+00	3.75e+00	2.50e+00	2.50e+00	2.50e+00	1.66e+00	1.10e+00	1.10e+00	7.26e-01	7.26e-0	4.77e-01	4.77e-01	2.03e-0	2.03e-01	8.55e-02	2.27e-02	5.88e-03	5.84e-04	1.41e-04

888	S E P P P P	RESULT ID O	Qy	뮻	Ma Bo	SO	DR	품:	3 ?	₽₽	RA A	₽?	8 8	R	88	8	S E	ဌ	ğ	5 5	5 8	RESULT
STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE; STREPTOCOCCUS.	01-AUG-1998 (TREMBLREL. 07, CREATED) 01-AUG-1998 (TREMBLREL. 07, LAST SEQUENCE UPDATE) 01-NOV-1998 (TREMBLREL. 08, LAST ANNOTATION UPDATE) GLUCOSYLTRANSFERASE-SI. GTFC.	UT 2 069391 PRELIMINARY; PRT; 1455 AA. 069391:	1 ANDHLSILEAWSDNDTPYLHD 21	507 ANDHLSILEAWSDNDTPYLHD 527	Query Match 100.0%; Score 148; DB 2; Length 1390; Best Local Similarity 100.0%; Pred. No. 8.69e-19; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 1390 AA; 155375 MW; C211E7B8 CRC32;	; D1027046	FEMS MICROBIOL. LETT. 161:331-336(1998).	Strentocomis mitans ".	S.;	н	MEDLINE; 98231643.	SEQUENCE FROM N.A.	[1]	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;	TOCOCCUS MUTANS.	GIFC.	. 08, LAST ANNOTATIO	07	1998 (TREMBLREL.	069385 PRELIMINARY; PRT; 1390 AA.	LT 1

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RESULT AC OCC SERVICE STATE OF SERVICE S
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STRAIN-MT4251;
STRAIN-MT4251;
MEDLINE; 98231643.
FUJIVARA T., TERAO Y
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MEDLINE: 98231643.
FUJIWARA T., TERAO Y., HOSHINO T., KIMURA S., HAWADA S.;
MOlecular analyse
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069381;
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"Molecular analyses of glucosyltransferase
Streptcoccus mutans.";
FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D88661; D1027054; -.
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MEDLINE; 98/31643.

FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA KIMURA S., HAMADA S.;

"Molecular analyses of glucosyltransferase of streptococcus mutans.";

Streptococcus mutans.";

FEMS. MICROBIOL. LETT. 161:331-336(1998).

EMBL; D88660; D1027053; -.
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01-AUG-1998 (TREMBLREL.
01-NOV-1998 (TREMBLREL.
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GLUCOSYLTRANSFERASE-I.
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MEDLINE; 9823
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                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-MT8148;
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BACTERIA; FIRMICUTES;
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                            glucosyltransferase
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Pred. No. 8.69e-19;
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FUJIWARA T., TERAO Y.
KIMURA S., HAMADA S.;
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FUJIWARA T., TERAO Y.,
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                                                                                                                                                                                                                                                                069397
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FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA KIMURA S., HAMADA S.;
KIMURA S., HAMADA S.;
"Molecular analyses of glucosyltransferase Streptococcus mutans.";
FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL; D88657; D1027049; -.
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FUJIWARA T., TERAO Y., HOSHINO T., KAWABATI KIMURA S., HAMADA S.;
"Molecular analyses of glucosyltransferase Streptococcus mutans.";
FEMS MICROBIOL. LETT. 161:331-336(1998).
EMBL: D89978; D1027060; -.
                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-MT4467;
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STRAIN-MT4239;
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GLUCOSYLTRANSFERASE-SI.
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"Molecular analyses of glucosyltransferase
Streptococcus mutans.";
FEMS MICROBIOL LETT. 161:331-336(1998).
EEMBL; D88652; D1027042; -.
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FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA S., C
KIMURA S., HAMADA S.;

"Molecular analyses of glucosyltransferase genes
Streptococcus mutans.";

FEMS MICROBIOL. LETT. 161:331-336(1998).

EMBL; D88658; D1027050; -
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FUJIWARA T., TERAO Y.,
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MEDLINE: 94146405.

SATO S., INOUE M., HANDA N., AIZAWA Y., ISOBE Y., KATAYAMA I SATO S., INOUE M., HANDA N., AIZAWA Y., ISOBE Y., KATAYAMA I SATO S., INOUE M., HANDA N., AIZAWA Y., ISOBE Y., KATAYAMA I SEQ. September of the glucosyltransferase gene of serotype d "DNA sequence of the glucosyltransferase gene of serotype d "Steptococcus sobrinus.";

DNA SEQ. 4:19-27(1993).

-i- CATAYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
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01-JAN-1999 (TREMBLREL 09, LAST ANN
GLUCOSYLTRANSFERASE-I PRECURSOR (EC
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STREPTOCOCCUS SOBRINUS.
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                                                         STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
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                              BACTERIA; FIRM
STREPTOCOCCUS.
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STRAIN-ATCC 33478;
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A; 175955 MW;
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                                                      BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
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(EC 2.4.1.5) (DEXTRANSUCRASE)
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RESULT 15

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DE GLUCOSYLTRAN;
GN GTFD.
OS STREPTOCOCCUS
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RN [1]
RP SEQUENCE FRO;
RR MEDILINE; 982;
RA KIMURA S., HI
RT "MOLECULIA"
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GLUCOSYLTRANSFEREASE-S.
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FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA
KIMURA S., HAMADA S.;
Molecular analyses of glucosyltransferase
        MEDLINE: 98231643.
FUJIWARA T., TERAO Y., HOSHINO T., KAWABATA
KIMURA S., HAMADA S.;
"MOLECULAR analyses of glucosyltransferase
                                                          SEQUENCE FROM N.A. STRAIN-MT4239;
                                                                                                         STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES;
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FUJIWARA T., TERAO Y.,
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                                                                                               STREPTOCOCCUS.
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"Molecular analyses of glucosyltransferase
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                                                                                                         BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

ar output not generated. Tue Jan 11 15:37:26 2000; MasPar time 2.42 Seconds 245.606 Million cell updates/sec

Run on:

Description: Perfect Score: Sequence: >US-09-290-049-1 (1-21) from US09290049.pep 148 1 ANDHLSILEAWSDNDTPYLHD 21

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37 1:swissprot

Statistics: Mean 29.534; Variance 43.172; scale 0.684

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

22211155 322118 322118	Result No.
148 131 131 131 101 101 101 64 64 65 65 65 65 65 65 65 65 65 65 65 65 65	Score
100 100 100 100 100 100 100 100 100 100	Query Match
13475 15925 14305 14305 14305 14306 14306 14316	Length I
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GTFB_STRMU GTFC_STRMU GTFS_STRDO GTFS_STRDO GTFS_STRMO G3PC_LEIME U116_STRMU G3PC_LEIME U126_STRMU FAS2_CANAL FCAS_CANAL FCAS_TRIGA KRAF_MSV36 KMIL_AVIMH KMIL_BVING KMIL_CHICK KMIL_CHICK KRAF_RAT KRAF_RAT KRAF_HUMAN SYDP_ECOLI G3PC_TRYBB G3P1_ECOLI	Ü
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39.2	39.2	39.2	39.2	39.9	39.9	39.9	39.9	39.9	39.9	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	41.2
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DELTA-(L-ALPHA-AMINOAD	GLYCERALDEHYDE 3-PHOSP	GLYCERALDEHYDE 3-PHOSP	GLYCERALDEHYDE 3-PHOSP	PUATIVE ATP-DEPENDENT	PERIODIC TRYPTOPHAN PR	INTERFERON REGULATORY	HYPOTHETICAL 31.5 KD P	GVPE PROTEIN, CHROMOSO	PUTATIVE GENE PROTEIN	TYROSINE-PROTEIN KINAS	PHOSPHATIDYLINOSITOL 3	PROBABLE ENDOCHITINASE	PROBABLE THREONYL-TRNA	HYPOTHETICAL 51.9 KD P	HOMEOBOX PROTEIN HOX-C	GLYCERALDEHYDE 3-PHOSP		MATING-TYPE PROTEIN AL	CYTOCHROME B6-F COMPLE	HYPOTHETICAL PROTEIN H	DEOXYRIBODIPYRIMIDINE
1.91e+01	1.91e+01	1.91e+01	1.91e+01	1.32e+01	1.32e+01	1.32e+01	1.32e+01	1.32e+01	1.32e+01	9.07e+00								9.07e+00		9.07e+00	6.21e+00

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EMBL; M17361; G153640; PIR; B33135; B33135. PFAM; PFO0128; alpha-amylase; 1. TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES. SIGNAL 1 34 POTENTIAL.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF GLUCANS. -i- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCANBINDING PROTEIN FROM S.MUTANS.	JOSE + (1.6-ALPHA-D-GLUCOSYL) (N) = OSE + (1.6-ALPHA-D-GLUCOSYL) (N+1). ULAR LOCATION: SECRETED. I DENTAL CARIES. INTHESIZES WAFER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKE) AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WAFER-SOLUBLE OFFICE OF THE STREET OF THE STR	N.A. 1013. 1013. 1014. 1015. 1015. 1017. 1018. 1019. 101	GTFB_STRMU STANDARD; PRT; 1475 AA. P08987; P08987; 01-NOV-1988 (REL. 09, CREATED) 01-NOV-1988 (REL. 09, LAST SEQUENCE UPDATE) 15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE) GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE) (SUCROSE 6-GLUCOSYLTRANSFERASE). STREPTOCOCCUS MUTANS. BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCUS. STREPTOCOCCUS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SHIROZA T., UEDA S., KURAMITSU H.K.;

SHIROZA T., UEDA S., KURAMITSU H.K.;

"Sequence analysis of the gifb gene from Streptococcus mutans.";

J. BACTERIOL. 169:4263-4270(1987).

-I. FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT OF PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUTOF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-I. CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) -

D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL) (N+1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P13470; P05427;
P13470; P05427;
O1-NOV-1988 (REL. 09, CREATED)
O1-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4.1.5) (GTF-SI)
GLUCOSYLTRANSFERASE) (SUCROSE 6-GLUCOSYLTRANSFERASE).
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                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                     EMBL; M22054; G153643; EMBL; M17361; G153641;
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BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
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nes 21; Conservation
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Pred. No. 1.49e-18;
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CATALLYIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
A REPEAT.
5 X TANDEM REPEATS.
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PF00128; alpha-amylase; P00695; 2HEE.

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GLYCOSYLTRANSFERASE;

SIGNAL; REPEAT; DENTAL CARIES

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SOF FITTER STATES OF THE STATES 
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Matches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus sobrinus glucosyltransferase (water-insoluble glucan synthetase).";

J. BACTERIOL. 173:989-996(1991).

-i- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-i- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) -
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                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as not removed modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                       EMBL; D90213; G217033; PIR; A38175; A38175.
                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
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ABO H., MATSUMURA T., KODAMA T., OHTA H.,
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SIGNAL
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Streptococcus sobrinus glucosyitransferase
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                                                                                                                                                                                                                                                                                               D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
SUBCELLULAR LOCATION: SECRETED.
DISEASE: DENTAL CARIES.
DISEASE: DENTAL CARIES.
GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-BINDING PROTEIN FROM S.MUTANS.
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GLYCOSYLTRANSFERASE; SIGNAL;
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BACILLUS/CLOSTRIDIUM GROUP;
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No. 1.10e-15;
                                                                                                                                            oved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                            There
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
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1 AC REPEATS.
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                                                                                                                                                                                          its content
                                                                                                                                                                                                                 are no
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                                                                                                                                                                                                                 restrictions
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                                                                                                                                                                                                                                   EMBL outstation
                                                                                                                                                                                                                                          a collaboration -
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                                                                                                between the Swiss institute. There are no to the European Bioinformatics Institute. There are no to the European Bioinformatics Institutions as long as its content is in no way use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
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01-JUL-1989 (REL. 11, LAST ESQUE
15-DEC-1998 (REL. 37, LAST ANNOT
GLUCOSYLTRANSFERASE-I PRECURSOR
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTF1
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CHAIN
                                                                 EMBL; M17391; G153647; - PFAM; PF00128; alpha-amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREPTOCOCCUS DOWNEI BACTERIA; FIRMICUTES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1989
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                                        SIGNAL
                                                    TRANSFERASE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence
                                                                                                                                                                                                                                                                                                          BACTERIOL. 169:4271-4278(1987).

FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAN OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
                                                                                                                                                                                                        GLUCANS.
SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES
BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                               GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
                                                                                                                                                                                                                                                                                       DISEASE: DENTAL CARIES.
                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: SECRETED.
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Similarity 85.7%;
18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  J.J., GILPIN
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                                                    GLYCOSYLTRANSFERASE;
                                                                   alpha-amylase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11, CREATED)
11, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
SE-I PRECURSOR (EC 2.4.1.5)
  38
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BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176167
                                                                                                                                                                                                                                                                                                                                                                                                                   ., RUSSELL R.R.B.;
glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 131; DB 1; Leux
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          497
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POTENTIAL.
GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLUCOSYLTRANSFERASE-I.
CATALYTIC (APPROXIMATE).
GLUCAN-BLUDING (APPROXIMATE).
6.5 X TANDEM REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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273A23FA CRC32;
                                                 SIGNAL; REPEAT; DENTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                   gene from Streptococcus
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                                                    CARIES
                                                                                                                                                                      a collaboration
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Matches 1
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REPEAT
                                                                                                                                                                                                                                                                                                     GILMORE K.S., RUSSELL R.R., FERRETTI J.J.;

"Analysis of the Streptococcus downed gtfs gene, which specifies a glucosyltransferase that synthesizes soluble glucans.";

INTECT. IMMUN. 58:2452-2458(1990).

-I- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT OF LAY A KEY ROLE IN THE DEVELOPMENT OF THE BUNTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

-I- CATALYTIC ACTIVITY: SUCROSE + (1,6 ALPHA-D-GLUCOSYL)(N) -

D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

-I- ENZYME REGULATION: GLUCAN SYNTHESIS BY GTF-S IS INDEPENDENT OF PRIMER GLUCAN UNLIKE GTF-I.
 DOMAIN
DOMAIN
DOMAIN
REPEAT
REPEAT
                                                               SIGNAL
CHAIN
                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLUCOSYLTRANSFERASE-S
(SUCROSE 6-GLUCOSYLTRA
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P29336;
01-DEC-1992 (REL
                                                                                                             EMBL; M30943; G153653; -. PIR; A41483; A41483.
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01-APR-1993 (REL.
                                                                                                   PIR; A41483; A41483.
PFAM; PF00128; alpha-amylase;
                                                                                        TRANSFERASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 90316665.
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                                                                                                                                                                                                                                                                 DISEASE: DENTAL CARIES.
GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND S
                                                                                                                                                                                                                                                        BINDING PROTEIN FROM S.MUTANS.
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18; Conser
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992 (REL. 24, LAST SEQUENCE UPDATE)
993 (REL. 25, LAST ANNOTATION UPDATE)
993 (REL. 25, LAST ANNOTATION UPDATE)
97RANSFERASE-S PRECUSOR (EC 2.4.1.5) (GTF-S)
6-GLUCOSYLTRANSFERASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIRMICUTES;
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                                                                                        GLYCOSYLTRANSFERASE;
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BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177080
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GLUCAN-BINDING (4.5 X TANDEM REI
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Pred. No. 1.66e-14;
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AC REPEAT.
B REPEAT.
AC REPEAT.
AC REPEAT.
AC REPEAT.
AC REPEAT.
                                               OR 37 (POTENTIAL).
GLUCOSYLTRANSFERASE-S.
CATALYTIC (APPROXIMATE)
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                                                                                     SIGNAL; REPEAT; DENTAL CARIES.
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                                                                                                                                                                                                                                                                  A 1,6-GLUCOSE).
SOME TO A GLUCAN
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Best Local
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Best Local
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SEQUENCE
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REPEAT
REPEAT
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01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5)
CSUCROSE 6-GLUCOSYLTRANSFERASE).
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                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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GTFD_STRMU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                          SIGNAL
                                                                                                                                                                                                                                                                                                         TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT;
                                                                                                                                                                                                                                                                                                                                                              EMBL; M29296; G153645; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 91100958.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREPTOCOCCUS MUTANS.
495 AINHLSILEAWSDNDPQY 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of the Streptococcus mutans gtfD gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e glucosyltransferase-S enzyme.";
GEN. MICROBIOL. 136:2099-2105(1990).
FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
OF THEIR ABILLTY TO ADHERE TO SMOOTH SURRACES AND MEDIATE THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
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14; Conser
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Pred. No. 6.06e-08;
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Best Local Similarity
Matches 10; Conser
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P03221;
21-JUL-1986
21-JUL-1986
15-DEC-1998
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15-JUL-1998 (RE)
GLYCERALDEHYDE
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INIT_MET
BINDING
ACT_SITE
SEQUENCE 3
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                                                                            EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS VIRUSES; DSDNA VIRUSES, NO RNA STAGE; HERPESVIRIDAE; GAMAHERPESVIRINAE; LYMPHOCRYPTOVIRUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G3PC_LEIME
Q01558;
SEQUENCE FROM N.A. MEDLINE; 84270667.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular analysis of the cytosolic and glycosomal phosphate dehydrogenase in Leishmania mexicana.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-SSP.
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PIR; B48445; B48445.
PROSITE; PS00071; GAPDH;
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HANNAERT V., BLAAN
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(REL. 28, LAST SEQUENCE UPDATE)
(REL. 36, LAST SEQUENCE UPDATE)
(DE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.12)
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01, LAST SEQUENCE UPDATE)
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175 A
35511 MW;
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BY SIMILARITY.
GLYCERALDEHYDE 3-PHOSPHATE.
ACTIVATES THIOL GROUP DURING
W; 80B6A7E9 CRC32;
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Pred. No. 7.25e-02;
3; Mismatches 6
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A SOUTHARD S.B., CIHLAR R.L.;

RA SOUTHARD S.B., CHILAR R.L.;

RT "Analysis and expression of the Candida albicans FAS2 gene.";

RL GENE 156:133-138(1995).

CC -!- FUNCTIONS: FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF

CC LONG-CHAIN FATTY ACID SYNTHETASE CATALYZES THE FORMATION OF

CC LONG-CHAIN FATTY ACID FROM ACETYL-COA, MALONYL-COA AND NADPH.

CC 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, AND 3-OXOACYL-[ACYL-CC CATALYTIC ACTIVITY: ACTYL-CCA+ N MALONYL-COA+ 2N NADPH =

CC CATALYTIC ACTIVITY: ACTYL-CARRIER PROTEIN] + MALONYL-[ACYL-CCC CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + MALONYL-[ACYL-CCC CATALYTIC ACTIVITY: ACYL-[ACYL-CARRIER PROTEIN] + CO(2) +

CC CATALYTIC ACTIVITY: (3R)-3-HYDROXYACYL-[ACYL-CARRIER PROTEIN] +

CC (ALBERIER PROTEIN] - 3-OXOACYL-[ACYL-CARRIER PROTEIN] +

CC (ALBERT PROTEIN] - 3-OXOACYL-[ACYL-CARRIER PROTEIN] +

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Best Local S
Matches
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EMBL; V0155; G59136; -.
EMBL; V717132; G243315; -.
PIR; A03784; QQBE40.
PIR; S33036; S33036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (REL. 32, CREATED)
01-NOV-1995 (REL. 32, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
FATTY ACID SYNTHASE, SUBGNIT ALPHA (EC 2.3.1.)
EC 1.1.1.100; EC 2.3.1.41)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GIBSON T.J., HATFULL G., HUDSON G.S., SATCHWELL S.C., SEGUIN
TUFFNELL P.S., BARRELL B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEN M.R., HSU T.Y., LIN S.W., CHEN J.Y., YANG C.S.; "Cloning and characterization of cDNA clones corresponding to transcripts from the BamHI G region of the Epstein-Barr virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EUKARYOTA; FI CANDIDACEAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CANDIDA ALBICANS (YEAST).
EUKARYOTA; FUNGI; ASCOMYCOTA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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GEN. VIROL. 72:3047-3055(1991).
SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL16,
HSV-6 ORFITR, EHV-1 46, HCMV UL94, EBV BDLF2, AND VZV 44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CANAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDHLSILEAWSDNDTP 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                336 AA;
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Query Match
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Q51508;
Q1-NOV-1997
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ACT_SITE
SEQUENCE
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15-DEC-1998
                                     PFAM; PF00
ISOMERASE.
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                 SERINO L., REIMMANN C., BAUR H., BE "Structural genes for salicylate bi Pseudomonas aeruginosa.", MOL. GEN. GENET. 249:217-228(1995).
                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ATCC 15692 / PAO1;
                                                                                                                                                                                                                                                                                                                                                                                                           PCHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00012; PHOSPHOPANTETHEINE; 1.
PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
FATTY ACID BIOSYNTHESIS; MULTIFUNCTIONAL ENZYME;
                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                 PSEUDOMONAS AERUGINOSA.
BACTERIA; PROTEOBACTERIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                MEDLINE; 96086939
                                                                                                                                                                                                                                                                                                                                                                                                                        SALICYLATE
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                                                                                                                                                                                                                                                                                                                                                                      SEUDOMONAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TWO MULTIFUNCTIONAL SUBUNITS (ALPHA & BETA).
SIMILARITY: TO THE FATTY ACID SYNTHETASE, SUBUNIT ALPHA FROM
OTHER FUNGI.
                                                                                                                                                                                                                                        FUNCTION: INVOLVED (PROBABLE).
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                                                                                                                                                                                                                              CATALYTIC
                                                                                                                                                                                         TRPE AND PABB.
                                                                                                                                                                                                                PATHWAY: SALICYLATE
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                                                X82644; G929780;
PF00425; chorisma
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Similarity 25.0%;
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35, LAST SEQUENCE UPDATE)
37, LAST ANNOTATION UPDATE)
THESIS ISOCHORISMATE SYNTHASE
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 Score 64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66;
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BETA-KETOACYL REDUCTASE.
BETA-KETOACYL SYNTHASE.
BETA-KETOACYL SYNTHASE.
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                                                                                                                                                                                                                                                      CONVERSION
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                          DEDC2D5C CRC32;
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No. 8.72e-01;
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 Length 476;
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(BY SIMILARITY).
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the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. Use entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
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MEDLINE; 90332429.
NEEPER M.P., JACOBSON M.A.;
"Sequence of a cDNA encoding the platelet aggregation inhibitor trigramin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRIMERESUROS GRAMINEUS (INDIAN GREEN TREE VIPER)
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; LEPIDOS
SCLEROGLOSSA; SERPENTES; COLUBROIDEA; VIPERIDAE;
TRIMERESURUS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1990 (REL. 14, GREATED)
01-AUG-1992 (REL. 23, LAST ANOOTATION UPDATE)
01-NOV-1995 (REL. 32, LAST ANOOTATION UPDATE)
PUTATIVE VENOM METALLOPROTEINASE PRECURSOR (EC 3.4.24.-) [CONTAINS:
                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUANG T.-F., HOLT J.C., KIRBY E.P., NIEWIAROWSKI S.; "Trigramin: primary structure and its inhibition of factor binding to glycoprotein IIb/IIIa complex on h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISINTEGRIN TRIGRAMIN ALPHA (PLATELET AGGREGATION INHIBITOR)].
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                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 408-419.
                                                                                                                                                                                                                                                                                                                                                                              "Platelet glycoprotein IIb-IIIa protein antagonists fr venoms: evidence for a family of platelet-aggregation PROC. NATL. ACAD. SCI. U.S.A. 87:2471-2475(1990).
                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                   DEISHER T.A., BUNTING S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-VENOM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEIC ACIDS RES. 18:4255-4255(1990)
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                                                                                                          METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUBFAMILY. SIMILARITY: HIGH, IN THE C-TERMINAL REGION, TO OTHER DISINTEGRINS.
                                                                                                                      SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B (ZINC METALLOPROTEASE); ALSO KNOWN AS THE REPROLYSIN SUB
                                     SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                 PROTEOLYTIC ACTIVITY.
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F., HOLT J.C.,
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                                                                                                                                                                                                                                                                                                                                                                                                                   PITTI R.M., LIPARI M.T., NAPIER M.A., LAZARUS R.A.;
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Mismatches 6;
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               (See http://www.isb-sib
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P09560; Q91390;
101-MAR-1989 (REL. 10, CREATED)
101-MAR-1989 (REL. 10, LAST SEQUENCE UPDATE)
15-JUL-1998 (REL. 36, LAST ANNOTATION UPDATE)
15-JUL-1998 (REL. 36, THREONINE-PROTEIN K
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   PIR; A29784; A29784.
PIR; A30065; A30065.
PROSITE; PS00142; ZINC_PROTEASE;
PROSITE; PS00427; DISINTEGRINS;
                                                                                                                                                                                                    XENOPUS LAEVIS (AFRICAN CLAWED FROG).
EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; AMPHIBIA; BATRACHIA; ANURA;
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                                                                                                      SEQUENCE FROM N.A. MEDLINE; 92096753.
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                                                                                              LE GUELLEC
                                                                                                                                MEDLINE; 89057471.
LEG GUELLEC R., LE GUELLEC K., PARIS J., PHILI
"Nucleotide sequence of Xenopus C-raf coding
NUCLEIC ACIDS RES. 16:10357-10357(1988).
                                                                                                                                                                    ISSUE-OOCYTE
                                                                            Xenopus c-raf proto-oncogene:
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European Bioinformatics Institute.

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EMBL; S74063; G241260; -.
PIR; S01930; TVXLRF
PROSITE; PS00107; PROTEIN_K
PROSITE; PS00108; PROTEIN_K
PROSITE; PS00479; DAG_PS_BI
PROSITE; PS00479; DAG_PS_BI
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DOMAIN
NP_BIND
BINDING
ACT_SITE
CONFLICT
              use by modified
                                                                                                                                                              WOLF A.H., SLAYMAN C.W., GRADMANN D.;

"Primary structure of the plasma membrane H(+)-ATPase from the halotolerant alga bunaliella bioculata.";

PLANT MOL. BIOL. 28:657-666(1995).

-i- FUNCTION: THE PLASMA MEMBRANE ATPASE OF PLANTS AND FUNGI IS A HYDROGEN ION PUMP. THE PROTON GRADIENT IT GENERATES DRIVES THE ACTIVE TRANSPORT OF NUTRIENTS BY H+-SYMPORT. THE RESULTING EXTERNAL ACIDIFICATION AND/OR INTERNAL ALKINIZATION MAY MEDIATE CONCERNAL ACIDIFICATION AND/OR INTERNAL ALKINIZATION MAY MEDIATE
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EUKARYOTA; VIRIDIPLANTAE; C
DUNALIELLACEAE; DUNALIELLA.
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01-OCT-1996
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PROSITE; PS00108; PROTEIN_KINASE_T; 1.
PROSITE; PS00479; DAG_PE_BINDING_DOMAIN;
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PFAM; PF00059; PKINASE; 1.
PFAM; PF00130; DAG_PE-bind; 1.
HSSP; P04049; 1FAO.
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            ween the Swiss Institute of Bioinformat
European Bioinformatics Institute. The
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                                                                                                             SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
                                                                                                                        CATALYTIC ACTIVITY: ATP + H(2)0 = ADP + ORTHOPHOSPHATE SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                (E1-E2 ATPASES).
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RANE ATPASE (EC 3.6.1.35) (PROTON
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PHORBOL-ESTER AND DAG
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http://www.isb-sib.ch/announce/
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P00532;
21-JUL-1986
21-JUL-1986
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                        PIR; A00638; TVMVF6.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS500118; PROTEIN_KINASE_ST; 1.

PROSITE; PS50011, PROTEIN_KINASE_DOM; 1.
                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-WOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
RAF SERINE/THREONINE-PROTEIN KINASE TRANSFORMING
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                                                                                                                    EMBL;
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SCIENCE 224:285-289(1984).
                                                                                                                                                                                                                                                                                                                                                                                                             MARK G.E., RAPP U.R.;
"Primary structure of v-raf:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A common onc gene sequence and by murine sarcoma virus SCIENCE 223:813-816(1984).
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-i- SIMILARITY: WITH THE CONSERVED CATALYTIC
-PROTEIN KINASES. BELONGS TO THE MIL/RAF S
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VIRUSES; RETROID VIRUSES;
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Best Local Similarity 30.0%;
Matches 6; Conservative
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BINDING
ACT_SITE
SEQUENCE
     CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                         KAN N.C., FLORDELLIS C.S., MARK G.E., DUESBERG P.H., PAPAS T.S.;

"A common one gene sequence transduced by avian carcinoma virus MH2
and by murine sarcoma virus 3611.";

SCIENCE 223:813-816(1984).

-I- DISEASE: BY ITSELF THE V-MIL ONCOGENE HAS ONLY WEAK TRANSFORMING
CAPACITY BUT IT ABOLLSHES THE GROWTH FACTOR REQUIREMENTS OF AVIAN
MACROPHAGES TRANSFORMED BY OTHER ONCOGENES.

-I- THIS PROTEIN IS SYNTHESIZED AS A GAG-MHT OR GAG-MIL POLYPROTEIN.

SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUL-1986 (REL. 01, CREATED)
21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
MIL SERINE/THREONINE-PROTEIN KINASE TRANSFORMING PROTEIN
(EC 2.7.1.-).
                                                    NP_BIND
                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                   EMBL; X00534; E235847; ALT_INIT. PIR; A00639; TVFVMM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 84121298.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Nucleotide sequence of avian retroviral oncogene v-mil: homologue of murine retroviral oncogene v-raf.";
NATURE 309:85-88(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE; 84191511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMIL_AVIMH
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                                                                                      DOMAIN
                                                                                                   TRANSFERASE;
                                                                                                                                   PFAM; PF00069;
HSSP; P11362; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BISTER K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUTRAVE P., BONNER T.I., RAPP U.R., JANSEN H.W., PATSCHINSKY T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V-MIL OR V-MHT.
AVIAN RETROVIRUS MH2.
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                                                                                                   ONCOGENE; ATP-BINDING
                                                                                                                  TRANSFORMING PROTEIN; SERINE/THREONINE-PROTEIN KINASE
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                                                                                                                                                    pkinase; 1.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
G -> E (IN REF. 2).
W; 1D7B2AB4 CRC32;
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ATP (BY SIMILARITY).
BY SIMILARITY.
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Pred. No. 4.23e+00;
7; Mismatches 7; Indels
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Query Match 41.9%; Score 62; DB 1; Length 380;
Best Local Similarity 30.0%; Pred. No. 4.23e+00;
Matches 6; Conservative 7; Mismatches 7; Indels 0; Gaps 0;
Db 146 TKDNLAIVTOWCEGSSLYKH 165
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Search completed: Tue Jan 11 15:37:35 2000 Job time: 9 secs.

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: ar output not generated. Tue Jan 11 15:47:05 2000; MasPar time 3.48 Seconds 253.134 Million cell updates/sec

Description: Perfect Score: Sequence: >US-09-290-049-3 (1-22) from US09290049.pep 155 1 TGARTINGQLLYFRANGVQYKG 22

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pirl 2:pir2 3:pir3 4:pir4

Statistics: Mean 29.032; Variance 42.944; scale 0.676

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

esult No.	Score	Query Match	Length	DB	Ħ	Description	Pred. No.
1	155	100.0	1475	2	взз135	gtfB protein precurso	4.92e-20
2	112	72.3	9	N	381	syltrans	5.30e-10
ω	109	70.3	\vdash	N	A44811		
4	107	69.0	1290	N	JC5473	dextransucrase (EC 2.	6.75e-09
5	106	68.4	1375	N	JT0345	8	.12e
6	106	68.4	1599	N	S22737	œ.	1.12e-08
7	104		1365	N	A41483	glucosyltransferase (3.05e-08
8	93	60.0	1431	N	A45866	dextransucrase (EC 2.	6.72e-06
9	88	56.8	563	N	A37184		7.21e-05
10	83	53.5	329	N	A55221	7	7.32e-04
11	79		382	N	S55166		4.46e-03
12	77		329	N	F71014	probable dipeptide tr	1.08e-02
13	72	46.5	126	N	S40016	doc protein - phage P	9.45e-02
14	71	45.8	425	N	H70410	191	1.44e-01
15	68	43.9	831	w	T00323	chitinase (EC 3.2.1.1	5.03e-01
16	67		245	N	F64465	cal p	7.58e-01
17	67	43.2	2710	N	A37052	\sim	7.58e-01
18	65	41.9	822	N	B54846	fibroblast growth fac	1.70e+00
19	65	41.9	1396	N	S36851	L-shaped tail fiber p	1.70e+00
20	63	40.6	240	N	H69366	conserved hypothetica	3.75e+00
21	63	40.6	301	N	S13165	asialoglycoprotein re	3.75e+00
22	63	40.6	310	ν	F71020	probable fructokinase	3.75e+00
23	63	40.6	396		WZBE8	dUTP pyrophosphatase	3.75e+00

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
60	60	60	60	60	60	60	60	60	61	61	61	61	61	62	62	62	62	63	63	63	63
38.7	38.7	38.7	38.7	38.7	38.7	38.7	38.7	38.7	39.4	39.4	39.4	39.4	39.4	40.0	40.0	•	•	•	•	40.6	•
788	788	738	696	648	513	483	473	472	613	440	402	336	244	2364	524	467	464	1082	566	475	404
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S25287	JS0747	160486	A29635	S10869	H71368	A71021	A33117	S17595	S74461	T02165	S32142	S09532	D70319	140884	S15619	S45493	S36501	P1XRPC	S74633	S65290	A54871
	regulatory protein Sp	gene trg protein – ra	transcription factor	enterotoxin A - Clost	hypothetical protein	hypothetical protein	cannabinoid receptor	id recepto	ABC-type transport pr	hypothetical protein	hypothetical protein	int protein - phage 1	uroporphyrin-III c-me	đ	otein – hu	isp6 protein - fissio	L2 protein - human pa	inner layer protein V	high affinity sulfate	clathrin-associated p	Gal beta-1, 3GalNAc-s
1.19e+01	1.19e+01	1.19e+01	1.19e+01	1.19e+01	1.19e+01	1.19e+01	1.19e+01	1.19e+01		8.12e+00		8.12e+00	8.12e+00	5.53e+00	5.53e+00	5.53e+00			•	3.75e+00	3.75e+00

Db 1300 TGARTING Qy 1 TGARTING RESULT 2 ENTRY 9 ORGANISM #	Query Match Best Local Simil Matches 22;		1289-1308 1354-1373	1096-1115 1224-1243		##experiment	##residues	##status ##molecule type		#authors S	REFERENCE	##restques	##molecule_type	S	#accession B	#title Sequ	#journal J		MISM		RESULT 1
TGARTINGQLLYFRANGVQVKG 1321	h 100.0%; Score 155; DB 2; Length 1475; Similarity 100.0%; Pred. No. 4.92e-20; 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	repeat homology #label olecular-weight 165811	repeat homology #label repeat homology #label	<pre>#domain cpl repeat homology #label CP1\ #domain cpl repeat homology #label CP2\</pre>	format speciment specimens.	##experimental_source strain GS-5		<pre>preliminary; not compared with conceptual translation voe DNA</pre>	A33128	Ueda, S.; Kuramitsu, H.K.	A33128	##Cross-references GB:M17361; NID:q153639; PID:q153640	DNA	preliminary		equence analysis of the gtfB gene from Streptococcus mutans.	J. Bacteriol. (1987) 169:4263-4270	23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change		B33135 #type complete	

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Best Local Similarity 77.3%;
Matches 17; Conservative
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Best Local Similarity 72.7%;
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1383 TGAQVINGQHLYFNADGSQVKG 1404
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1 TGARTINGQLLYFRANGVQVKG 22
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##cross-references EMBL:Z11873; NID:g47526; PID:g47527
##note sequence extracted from NCBI backbone
NCBIP:81052)
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glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius
#formal_name Streptococcus salivarius
31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
09-Sep-1997
A44811
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J. Gen. Microbiol. (1991) 137:2577-2593
Molecular characterization of a cluster of at least two
glucosyltransferase genes in Streptococcus salivarius ATCC
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glycosyltransferase; hexosyltran
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J. Bacteriol. (1991) 173:989-996
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#molecular-weight 167730 #ch
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Pred. No. 2.45e-09;
2; Mismatches 4
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Pred. No. 5.30e-10;
2; Mismatches 3;
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Best Local
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                                                                                                                                                                                                                                                                                                                                       #authors
#journal
#title
                                                                                                                                     #accession
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#description
                                                                                                                                 #authors Shiroza, T.; Ueda, S.; Kuramitsu, H.K. #journal J. Bacteriol. (1987) 169:4263-4270 #title Sequence analysis of the gtfB gene fro #cross-references MUID:87308013 #accession C33135
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                                                                                                ##molecule_type DNA
                                                                                                                                                                                                                                     ##experimental_source GS-5
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                                                                ##cross-references GB:M17361
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Local Similarity 63.6%;
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#formal_name Streptococcus mutans
31-Mar-1992 #sequence_revision 31-Mar-1992
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catalyzes the synthesis
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#domain glucan-binding #status predicted #label
#length 1290 #molecular-weight 145572 #checksum 93
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Gene (1988) 69:101-109
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(strain GS-5)
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#formal_name Leuconostoc mesenteroides
07-Jul-1997 #sequence_revision 29-Aug-1997
29-Aug-1997
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Pred. No. 6.75e-09;
3; Mismatches 5
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of both water-soluble and
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##residues 1-51 ##label
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##cross-references EMBL:Z11872; NID:g47530; PID:g47531
##experimental_source ATCC 25975
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A41483
Gilmore,
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glucosyltransferase (EC 2.4.1.-) gtfs precursor -
Streptococcus sobrinus
#formal_name Streptococcus sobrinus
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
09-Sep-1997
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J. Gen. Microbiol. (1991) 137:2577-2593
Molecular characterization of a cluster of at least two
glucosyltransferase genes in Streptococcus salivarius AF
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glycosyltransferase; hexosyltransferase
#length 1599 #molecular-weight 176480
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S22726
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#superfamily cpl repeat homology
duplication; glycosyltransferase; hexosyltransferase;
transferase
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16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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glucosyltransferase (EC 2
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#th 1375 #molecular-weight 153021 #checksum
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#PTOCUCT glucosytransferase #status predicted #label
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77.3%;
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             K.S.;
             Russell,
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Pred. No. 1.12e-08;
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Pred. No. 1
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           R.R.B.;
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L.12e-08;
           Ferretti,
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#cross-references MUID:90316665
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##molecule_type DNA
##residues 1-1431 ##label HON
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##residues 1-1365 ##label GIL
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Similarity 59.18;
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Similarity 63.6%;
14; Conservative
        A37184
A37184
Banas, J.A.; Russell,
Infect. Immun. (1990)
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glycosyltransferase; hexosyltran
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jth 1431
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Pred. No.
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          R.R.B.; Ferretti,
58:667-673
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##cross-references GB:M30943; NID:g153652; PID:g153653
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dextransucrase (EC 2.4.1.5) previous mutans allowers mutans allowers mutans allowers and sequence_revision 30-Sep-1993 #text_change 07-Jul-1995
A37184 #type complete
glucan-binding protein - Streptococcus mutans
#formal_name Streptococcus mutans
31-Jan-1992 #sequence_revision 31-Jan-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Honda, O.; Kato, C.; Kuramitsu, H.K.
J. Gen. Microbiol. (1990) 136:2099-2105
Nucleotide sequence of the Streptococcus mutans gtfD
encoding the glucosyltransferase-S enzyme.
A45866
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*superfamily cpl repeat homology
glycosyltransferase; hexosyltransferase
#length 1365 #molecular-weight 151590
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Analysis of the Streptococcus downei gtfS gene, which specifies a glucosyltransferase that synthesizes soluble
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#domain cpl repeat homology #label Cp2\
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Pred. No. 3.05e-08;
5; Mismatches 3
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tches 1
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349-368
504-523
525-548
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                      #description
                                       #submission
                                                        #authors
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Similarity 68.2%;
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Similarity 68.4%;
13; Conservative
 Katsoulou, C.; Tzermia, M.; Alexandraki, D. submitted to the EMBL Data Library, May 195. The complete sequence of a 40.7 kb segment loleft arm of yeast chromosome x identified ]
                                                                     $55166; $56929; $71650
$55159
                                                                                                                hypothetical protein J0639

#formal_name Saccharomyces cerevisiae
08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
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#length 329 #molecular-weight 36077 #chec
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Pred. No. 7.21e-05;
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#cross-references MUID:98344137
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##residues 1-382 ##label KAW
##cross-references EMBL:Z49422; NID:g1015560; PID:g1015561; MIPS:YJL147c
##CCC $71643
                                                 ##residues 1-329 ##label KAW
##cross-references GB:AP000006; NID:g3236133; PID:d1031461;
##experimental_source strain OT3
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##note the nucleotide sequence was submitted to
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Similarity 38.9%;
                                                                                                                                                                                                                                                                                                                       Hino, Y.; Yamamoto, S.; Sekine, M.; Baba, S.; Kosugi, H.;
Hosoyama, A.; Nagai, Y.; Sakai, M.; Ogura, K.; Otsuka, R.;
Nakazawa, H.; Takamiya, M.; Ohiku, Y.; Funahashi, T.;
Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
A.; Aoki, K.; Yoshizawa, T.; Nakamura, Y.; Robb, F.T.;
Horikoshi, K.; Masuchi, Y.; Shizuya, H.; Kikuchi, H.
DNA Res. (1998) 5:55-76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence analysis of a 40.7 kb segment from the left arm yeast chromosome X reveals 14 known genes and 13 new op reading frames including homologues of genes clustered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the Protein $556929
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                                                                                                                                                                                                                                                                           Complete sequence and gene organization of the genome of hyper-thermophilic archaebacterium, Pyrococcus horikosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable dipeptide transport ATP-binding Pyrococcus horikoshii
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                                                                                                                                                                                                       F71014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #formal_name Pyrococcus horikoshii
14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.;
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                                                                                                                                                   preliminary; nucleic acid sequence translation not shown
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                         this accession replaces an interim accession
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sequence replaced
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  by GenBank
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Best Local Similarity 44.4%;
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45-53
185-189
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#journal J. Mol. Biol. (1993) 233:414-428
#title Plasmid addiction general bacteriophage Pl: doc, which
causes cell death on curing of prophage, and phd, which
prevents host death when prophage is retained.
#cross-references MUID:94016561
   #journal #title
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#residues 26-126 ##label SCH
##cross-references EMBL:M95666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schmidt, C.; Lehnherr, H.; Guidolin, A.; Arber, W. submitted to the EMBL Data Library, November 1992 Additional late promoter sequences of bacterionham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP; binding protein-dependent transport system; nucleotide binding; oligopeptide transport; P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #superfamily inner membrane protein malk;
                 Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Overbeek, R.; Snead, M.A.; Keller, M.; Aulay, M.; Huber, R.; Feldman, R.A.; Short J.M.; Olson, G.J.; Swanson, R.V.
Nature (1998) 392:353-358
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                                                                                                                                                                                                            H70410 #type complete
UDP-N-acetylglucosamine 1-carboxyvinyltransferase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           doc protein - phage P1
#formal_name phage P1
25-pec-1994 #sequence_revision 17-May-1996 #text_change
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                                                                                                                                                                                 #formal_name Aquifex aeolicus
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complete genome of the hyperthermophilic bacterium
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#region
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#region nucleotide-binding motif A (P-loop)\
#region nucleotide-binding motif B
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56.3%;
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Pred. No. 1.08e-02;
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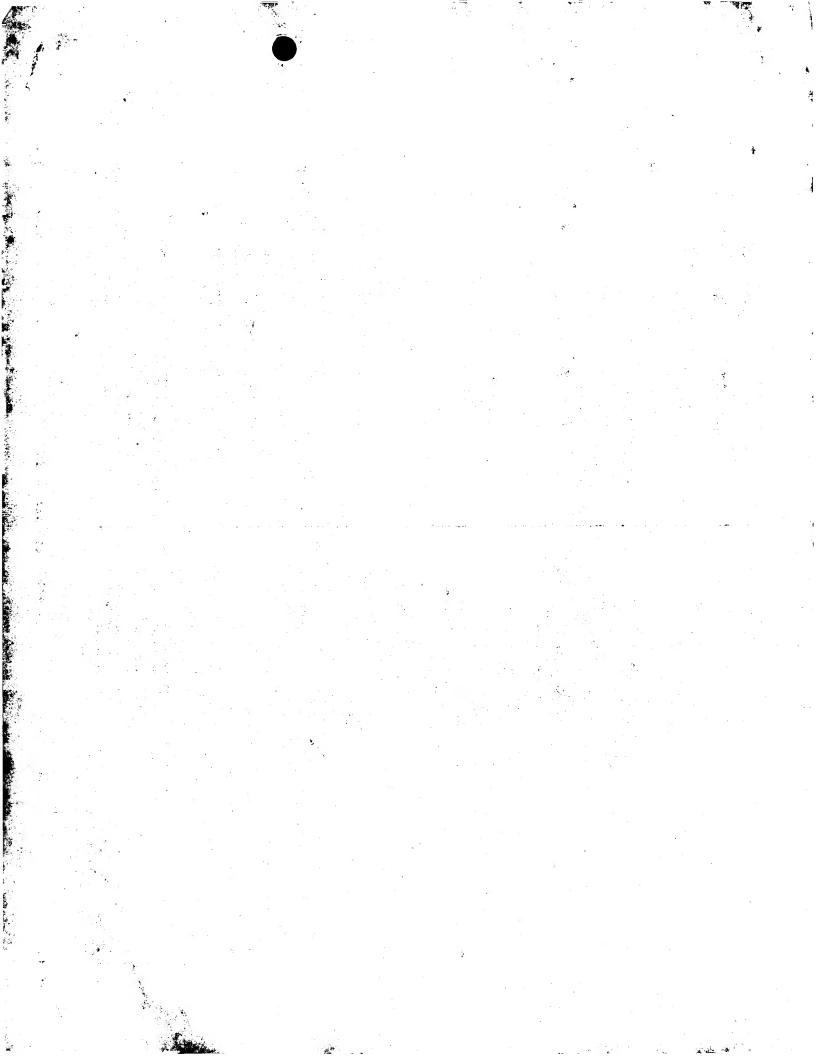
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#journal
#title
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Y #length
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Local Similarity 42.1%;
ses 8; Conservative
                                                                              Match 43.98;
Local Similarity 36.48;
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TGARTINGQLLYFRANGVQVKG
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                                TAAKTVKNMKVYIKTNGVAITG 546
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1-carboxyvinyltransferase MurZ
#length 425 #molecular-weight 47259
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                                                                                                                                                                                                                        Cloning, sequencing, and expression of the gene encoding Clostridium paraputrificum chitinase ChiB and analysis the functions of novel cadherin-like domains and a
                                                                                                                                                                                                                                                                                                                                                  700323 #type complete
chitinase (EC 3.2.1.14) B - Clostridium paraputrificum
#formal_name Clostridium paraputrificum
29-Jan-1999 #sequence_revision 29-Jan-1999 #text_change
                                                                                                                                                                                                                                                                      Ohmiya, K.; Sakka, K.; Kimura, T.; Karita, S.; Morimoto, J. Bacteriol. (1997) 179:7306-7314
                                                                 Conservative
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                                                                                                                                                                                                           chitin-binding domain.
                                                                                                                            preliminary
1-831 ##label OHM
2-85 EMEL:AB001874; NID:dl175645;
3th 831 #molecular-weight 90021
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   22
                                                                                Score 68; DB 3;
Pred. No. 5.03e-01
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Pred. No. 1.44e-01;
5; Mismatches 6
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:36:55 2000; MasPar time 3.63 Seconds 232.086 Million cell updates/sec

ar output not generated.

Description: Perfect Score: Sequence: Title: >US-09-290-049-1 (1-21) from US09290049.pep 148

1 ANDHLSILEAWSDNDTPYLHD 21

Scoring table: PAM 150 Gap 15

Searched: 122810 seqs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 28.783; Variance 46.009; scale 0.626

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

222118 322210 32210 32210	Result No.
148 136 1021 1031 1031 1031 1031 1031 1031 1031	Score
100 0 91 9 68 9 50 7 50 7 44 8 6 43 2 44 2 6 41 9 41 9	Query
1475 1595 1596 1599 15189 15189 15189 331 336 490 485 542 548 548 548 548 548 548 548 548 548 548	Length I
HHHH0H0000H00000000	BB
B33135 A318175 A318175 A41483 A42866 S22737 A44811 B48445 CQBE40 E71557 H70538 S7C4086 S7C4086 S7C4086 S7C4086 TVC2301 TVX1RF S34213 TVVMM TVRTRF S00644 TVRTRF	Ħ
gtfB protein precurso dextransucrase (EC 2. glucosyltransferase p glucosyltransferase (EC 2. glucosyltransferase (EC 2. glucosyltransferase (glucosyltransferase (glucosyltransferase (glyceraldehyde-3-phos BGLF2 protein - human hypothetical protein probable ppdK protein fatty-acid synthase (poha protein - Pseudotrigramin precursor - probable PSII Dl protaldehyde dehydrogenas protein kinase raf-1 H+transporting ATPas protein kinase (EC 2. protein kinase (EC 2. protein kinase (EC 2. protein kinase raf-1 protein kinase raf-1 protein kinase raf-1	Description
7.09e-17 3.13e-14 3.813e-14 3.813e-14 3.819e-07 1.70e-02 5.82e-02 1.94e-01 1.94e-01 1.94e-01 1.94e-01 1.94e-01 1.94e-00 4.19e+00 4.19e+00 4.19e+00 4.19e+00 6.06e+00 6.06e+00 8.72e+00 8.72e+00 8.72e+00 8.72e+00 8.72e+00 8.72e+00	Pred. No.

JT0345 #type complete dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans (strain GS-5)

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24
59	60	60	60	60	60	60	60	60	60	60	60	60	60 .	60	13	61	61	61	61	61	62
39.9	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	40.5	41.2	41.2	41.2	41.2	41.2	41.2	41.9
481	1177	1066	692	664	535	471	353	342	337	221	210	184	181	116	1581	481	331	331	202	181	648
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JC4342	A36984	F71100	H70362	PC4002	S76564	S66829	E64641	A56552	C64233	F64858	JFBYA2	JC2104	S38460	C64017	B71636	B32580	DEUTGC	DEECG3	HYTVH2	A55944	TVHUF6
fibrinolytic proteina	protein-tyrosine kina	probable isoleucyl-tR	glycogen phosphorylas	<pre>phosphatidylinositol-</pre>	hypothetical protein	probable membrane pro	hypothetical protein	homeotic protein Hox-	glyceraldehyde-3-phos	ymfD protein - Escher	mating-type regulator	hypothetical 20.8K pr	plastoquinolplastoc		hypothetical protein	deoxyribodipyrimidine	glyceraldehyde-3-phos	glyceraldehyde-3-phos	hemorrhagic protein H	syd protein - Escheri	protein kinase raf-1
2.54e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.78e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	1.25e+01	8.72e+00

ALIGNMENTS

RESULT 2 ITTLE dextrain GS-5) (etrain GS-5)	Db 481 ANDHLSILEAWSDNDTPYLHD 501 	Query Match 100.0%; Score 148; DB 2; Best Local Similarity 100.0%; Pred. No. 7.09e-17; Matches 21; Conservative 0; Mismatches 0	-1115 #domain cpl repeat -1243 #domain cpl repeat -1308 #domain cpl repeat -1373 #domain cpl repeat -1438 #length 1475 #molecular	##residues 1-171,173-641,'N',643-1475 ##experimental_source strain GS-5 CLASSIFCATION #superfamily cpl repeat homology	##status	rs Shir ssion subm	##residues 1-1475 ##Label SHI ##cross-references GB:M17361; NID:g153639; PID:g153640	s ule_type	#trite sequence analysis of the gui #cross-references MUID:87308013 #accession B33135	rs Shiroza, T.; Ueda, S.; al J. Bacteriol. (1987) 1	ACCESSIONS B33125; A33128 REFERENCE A33135	RESULT 1 B33135 #type complete ENTRY 9tfB protein precursor - Streptococcus mutans ORGANISM #formal_name Streptococcus mutans DATE 23-Oct-1990 #t
precursor - Streptococcus mutans		DB 2; Length 1475; .09e-17; ches 0; Indels 0; Gaps 0;	homology #label CP1\ homology #label CP2\ homology #label CP3\ homology #label CP4\ homology #label CP5\ homology #label CP5 -weight 165811 #checksum 7497	1475 ##label SH2 ology	red with conceptual translation	mitsu, H.K. quence Database, September 1990	639; PID:g153640		is gene from Streptococcus mutans.	H.K.		reptococcus mutans mutans ion 23-Oct-1990 #text_change

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1253-1272
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#title
                                                                                                              #title Peptide sequences for sucrose splitting and glucan binding within Streptococcus sobrinus glucosyltransferase (water-insoluble glucan synthetase).

#cross-references MUID:91123227
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#journal J. Bacteriol. (1987) 169:4263-4270
#title Sequence analysis of the gtfB gene fro
cross-references MUID:87308013
                                                                                                                                                                                                                                                                                                                                                                                                              507 ANDHLSILEAWSYNDTPYLHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ##status preliminary
##molecule_type DNA
##residues 1-349 ##label
##cross-references GB:M17361
                              ##cross-references GB:D90213; NID:g217032; PID:d1014946; PID:g217033
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#formal_name Streptococcus muta
31-Mar-1992 #sequence_revision
22-Nov-1996
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larity 95.2%;
Conservative
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#superfamily cpl repeat homology
duplication; glycosyltransferase; hexosyltransferase;
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                #superfamily cpl repeat homology
                                                                                                                                                                                J. Bacteriol. (1991) 173:989-996
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##cross-references GB:M29296
(FICATION #superfamily cpl repeat homology glycosyltransferase; hexosyltran
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                                                    ##residues
                                                                        ##molecule_type DNA
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##cross-references GB:M30943; |
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Local Similarity 85.7%;
nes 18; Conservation
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Local Similarity 71.4%;
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dextransucrase (EC 2.4.1.5) precursor - Streptococcus mu
#formal_name Streptococcus mutans
30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
07-Jul-1995
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#length 1592
                                                                                                                       Honda, O.; Kato, C.; Kuramitsu, H.K.
J. Gen. Microbiol. (1990) 136:2099-2105
Nucleotide sequence of the Streptococcus mutans gtfD
Nencoding the glucosyltransferase-S enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Infect, Immun. (1990) 58:2452-2450
Analysis of the Streptococcus downei gtfS gene, which
specifies a glucosyltransferase that synthesizes soluble
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glycosyltransferase; hexosyltransferase
#length 1365 #molecular-weight 151590
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Analysis of the Streptococcus downei gtfS
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Pred. No. 4.40e-07;
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Pred. No. 3.81e-13;
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#cross-references EMBL:Z11872; NID:g47530; PID:g47531
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14; Conservative
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#superfamily cpl repeat homology
glycosyltransferase; hexosyltransferase
#length 1599 #molecular-weight 176480
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Molecular characterization of a cluster of at least two glucosyltransferase genes in Streptococcus salivarius AT(25975.
                          Giffard, P.M.; Simpson, C.L.; Milward, C.P.; Jacques, N. J. Gen. Microbiol. (1991) 137:2577-2593

Molecular characterization of a cluster of at least two
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S22726
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glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius
#formal_name Streptococcus salivarius
31-pec-1993 #sequence_revision 31-pec-1993 #text_change
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glucosyltransferase (EC 2.4.1.-) S - Streptococcus salivarius
#formal_name Streptococcus salivarius
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Pred. No. 6.99e-07;
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             #cross-references MUID: 93063042
#accession B48445
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##molecule_type DNA
##residues 1-1518 ##label GIF
##cross-references EMBL:Z11873; NID:g47526; PID:g47527
##cross-references extracted from NCBI backbone (NCBIN:81050,
##note NCBIP:81052)
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##molecule_type DNA
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##cross-references EMBL:x65220; NID:g9552; PID:g9553
#FICATION #superfamily glyceraldehyde-3-phosphate decouple oxidoreductase
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Similarity 52.6%;
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Similarity 66.7%;
10; Conservative
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BGLF2 protein - human herpesvirus 4 (strain B95-8)
#formal_name human herpesvirus 4, Epstein-Barr virus
25-Feb-1985 #sequence_revision 25-Feb-1985 #text_change
22-Jan-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hannaert, V.; Blaauw, M.; Kohl, L.; Allert, S.; Opj
F.R.; Michels, P.A.M.
Mol. Biochem. Parasitol. (1992) 55:115-126
Molecular analysis of the cytosolic and glycosomal
glyceraldehyde-3-phosphate dehydrogenase in Leisl
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#superfamily cpl repeat homology
glycosyltransferase; hexosyltransferase
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31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
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Pred. No. 5.82e-02;
2; Mismatches 3
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**cross references EMBL:V01555; NID:g59074; PID:g1334895

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       title Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.

*cross-references MUID:99000809

*accession E71557
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#journal J. Gen. Virol. (1991) 72:3047-3055

*title Cloning and characterization of CDNA clones corresponding transcripts from the BamHI G region of the Epstein-Barr virus genome and expression of BGLF2.

Cross-references MUID:92113548
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##cross-references GB:S77132; NID:g243314; PID:g243315
#FICATION #superfamily Epstein-Barr virus BGLF2 protein
RY #length 336 #molecular-weight 36888 #checksum
                                                                                                                                                             132 QLPMLTSWPEDGGPFL 147
                                                                                                                                                                                                                                                                                                                                                         ##status preliminary
##molecule_type DNA
##residues 1-579 ##label ARN
##cross-references GB:AE001283; GB:AE001273; NID:g3328480;
##experimental_source serotype D, strain UW-3/Cx
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                                                                                                                    4 HLSILEAWSDNDTPYL
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probable
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, W.P.; Olinger, L.; Tatusov, R.L.; Zhao, O.; Koonin, E.V.; Davis, R.W.
Science (1998) 282:754-759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation; protein coding region neither amino acid nor nucleotide sequence is given
                                                                                                                                                                                                                                                                                              *length 579 *molecular-weight 65354 *checksum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   #formal_name Chlamydia trachomatis
13-Sep-1998 #sequence_revision 13-Sep-1998
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hypothetical protein CT085 - Chlamydia trachomatis (serotype
                                                                                                                                                                                                           Conservative
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#type complete
ppdK protein - Mycobacterium
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                                                                                                                                                                                                       Score 72; DB 2; Pred. No. 1.94e-01 8; Mismatches
                                                                                                                                                                                                                                                  Length 579;
    tuberculosis (strain
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SUMMARY
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1299-1304
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Query Match 44.6%;
Best Local Similarity 25.0%;
Matches 5; Conservative
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #authors Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.V.; Eiglmeier, K.; Gas, S.; Barry III, C.E.; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, S.; Osborne, J.; Quail, M.A.; Moule, S.; Mandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Selton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Skelton, S.; Squares, S.; Sqares, R.; Sulston, J.E.; Faylor, K.; Whitehead, S.; Barrell, B.G. Nature (1998) 393:537-544

Beciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                    #title Analysis and expression
#cross-references MUID:95255657
                                                                                                                                                                                                                                                #gene
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Similarity 57.1%;
8; Conservative
                                                                                                                                                                                                                               fas2
                                                                                                                                                                                                                                                                                                                                                                                           Southard, S.B.; Cihlar, Gene (1995) 156:133-138
                                                                                                                                                                               *superfamily yeast fatty-acid synthase acyltransferase; fatty acid biosynthesis; phosphopantetheine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #formal_name Candida albicans
12-Jul-1995 #sequence_revision
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17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change
17-Jul-1998
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fatty-acid synthase (EC 2.3.1.85) alpha chain -
(Candida albicans)
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#length 490 #molecular-weight 52004
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                                                                         #length 1885
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                                                                                                                                                                     phosphoprotein
                                                                                                           #region cerulenin binding #status predicted\
#binding_site phosphopantetheine (Ser) (covalent)
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translation not shown
                                                                                            #status
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                                                                         #molecular-weight 207588 #checksum
                                                                                        predicted
Pred.
8; 1
                   Score 66; DB 2; I
Pred. No. 1.98e+00;
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Pred. No. 1.36e+00;
4; Mismatches 2;
 Mismatches
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Best Local Similarity 47.18;
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#title
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#title
                                                                                                                                                                                                                                                                                                                                                                                                        *authors Neeper, M.P.; Jacobson, M.A.
journal Nucleic Acids Res. (1990) 18:4255
*title Sequence of a cDNA encoding the platelet aggregation
trigramin.
*cross-references MUID:90332429
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##note this protein is involved in salicylate biosynthesis
FICATION #superfamily isochorismate synthase
#length 476 #molecular-weight 52071 #checksum 7909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ##molecule_type DNA
                                                           ##molecule_type protein
##residues 408-479 ##label HUA
                                                                                                                                                                                                                                                                           ##residues 1-480 ##label NEE
##cross-references EMBL:X51530; NID:964407; PID:964408
##note translation of the signal sequence and
protein but not of the propeptide is
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Huang, T.F.; Holt, J.C.; Lukasiewicz, H.; J. Biol. Chem. (1987) 262:16157-16163
                                                                                                                                                 Trigramin: primary structure and its inhibition of von Willebrand factor binding to glycoprotein IIb/IIIa complex on human platelets.
                                                                                                                                                                                                                Huang, T.F.; Holt, J.C.; Kirby, E.P.; Niewiarowski, Biochemistry (1989) 28:661-666
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S12589
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Structural genes for salicylate biosynthesis from chorismate
                                        A29784
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13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
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Pred. No. 4.19e+00;
3; Mismatches 6
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Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.;

Dean, C.; Bergkamp, R.; Dirkse, W.; Van Staveren, M.;

Stiekema, W.; Drost, L.; Ridley, P.; Hudson, S.A.; Patel,
K.; Murphy, G.; Piffanelli, P.; Wedler, H.; Wedler, E.;

Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.;

Gielen, J.; Villarroel, R.; De Clerck, R.; Van Montagu, M.;

Lecharny, A.; Auborg, S.; Gy, I.; Krets, M.; Lao, N.;

Kavanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger,
M.; Schaeffer, M.; Funk, B.; Mueller-Auer, S.; Silvey, M.;

James, R.; Wontfort, A.; Pons, A.; Pulgdomenech, P.; Douka,
A.; Voukelatou, E.; Milioni, D.; Hatzopoulos, P.;

Piravandi, E.; Obermaier, B.; Hilbert, H.; Duesterhoft, A.;

Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.;

Rechman, S.; Ansorge, W.; Cooke, R.; Berger, C.; Delseny,
M.; Voet, M.; Volkaert, G.; Mewes, H.W.; Klosterman, S.;

*journal Nature (1998) 391:485-488

*title of Analysis of 1.9 Mb of contiguous sequence from chromosome 4

*cross-references MUID:98121113

*accession E71447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
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Best Local Similarity
                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 43.2%;
Best Local Similarity 63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             398-476
408-479
458-460
279
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334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #variety
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                                                                           #map_position 4COP9-4G3845
MARY #length 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #cross-references MUID:88058981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ##molecule_type protein
##residues 408-419 ##label HU2
##residues #superfamily trigramin precursor; disintegrin homology
ADS anticoagulant; glycoprotein; hydrolase; metalloproteinase;
venom; zinc; zymogen
                                                                                                                                                      ##residues 1-515 ##label BEV
##cross-references GB:Z97344; NID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  244 LSVLEIWSEKD 254
                                                                                                                                                                                                       ##molecule_type DNA
                                                                                                                                                                                                                                                             ##status
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fibrinogen interaction with platelet receptors expressed
glycoprotein IIb-IIIa complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Arabidopsis thaliana #common_name mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E71447 #type complete
probable PSII D1 protein processing enzyme - Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #length 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             thaliana
                                                                                                                                                                                                                               preliminary; nucleic acid translation not shown
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binding_site zinc (His) #status p
binding_site giu #status predicted
active_site Glu #status predicted
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#domain disintegrin homology #label DIS\
#product trigramin #status experimental #label MAT\
#region cell attachment (R-G-D) motif\
#binding_site carbohydrate (Asn) (covalent) #status
43.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #molecular-weight 53494 #checksum 1021
                                                                           #molecular-weight 55762 #checksum 303
Score 64; DB 2; I
Pred. No. 4.19e+00;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 64; DB 1; I
Pred. No. 4.19e+00;
                                                                                                                                                    NID:g2245126; PID:e327081; PID:g2245133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                          Length 515;
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Search completed: T Job time : 14 secs.	Qy	đ	Mat
h cor ime	1	128	Matches
nplet : 14	ANDH	TEEN	
ed:	LSIL	LLFL	7;
Search completed: Tue Jan 11 15:37:09 2000 Job time : 14 secs.	ANDHESILEAWSDNDTPYL 19	128 TEENLLFLEAWRTIDRAYI 146	7; Conservative
37:0		<u>o</u>	7;
2000			7; Mismatches 5; Indels 0; Gaps 0;
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			Indels
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(MT)	***

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Run on: MPsrch_pp protein - protein database search, using Smith-Waterman algorithm Tue Jan 11 15:46:28 2000; MasPar time 3.84 Seconds 121.776 Million cell updates/sec

Sequence: Description: Perfect Score: Title: >US-09-290-049-3 (1-22) from US09290049.pep 155 1 TGARTINGQLLYFRANGVQVKG 22

ar output not generated.

Scoring table: PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38 24:part24 29:part29 34:part34 39:part39

Mean 20.775; Variance 64.431; scale 0.322

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Re																	
Result No.	בן	J		ω	4	Ç,	σ	7	œ	9	10	11	12	13	14	15	16
Score	114	114	TT4	114	112	88	67	67	67	67	63	62	61	61	60	60	60
Query Match		72 5	70.0	73.5	72.3	56.8	43.2	43.2	43.2	43.2	40.6	40.0	39.4	39.4	38.7	38.7	38.7
Length	22	J J	2.2	24	1592	1577	811	812	2710	2710	404	349	207	514	116	472	473
DB	25	œ	o	25	σ	16	17	17	17	35	16	19	34	39	19	ω	ω
ij	W34159	202510	X43090	W34164	R32925	R91047	R95014	R95017	R95016	W68387	R78621	W06416	W38549	W83359	W03642	R14196	R14195
Description	GTF antiqenic peptide	3	GI subsequence.	GTF antigenic peptide	Glucosyltransferease	Alpha-D-glucosyltrans	C. difficile toxin A	C. difficile toxin A	C. difficile toxin A.	Clostridium difficile	Chicken GalNAc-alpha-	Phosphotriesterase-re	S. pneumoniae peptide	Streptococcus pneumon	Human cannabinoid GPR	Human cannabinoid rec	Rat cannabinoid recen
Pred. No.	4.41e-05	41000	4.41e-05	4.41e-05	7.62e-05	4.64e-02	9.21e+00	9.21e+00	9.21e+00	9.21e+00	2.40e+01	3.04e+01	3.85e+01	3.85e+01	4.87e+01	4.87e+01	4 87e+01

	45	44	43	42	4	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
	54	54	55	55	55	55	55	55	56	56	56	56	56	56	56	57	57	57	57	57	58 8	59	59	59	59	59	59	59	59	
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	2366	667	1657	1139	503	485	449	265	486	450	448	432	336	336	15	572	501	501	492	488	1301	998	998	673	453	453	453	233	91	
	17	28	24	37	N	ω	12	28	22	σ	ø	σ	σ	σ	9	œ	ω	15	ഗ	IJ	σ	15	19	13	35	20	10	13	17	
	R95011	W44701	W18822	W76425	P70219	R13513	R66742	W46518	W20586	R30738	R49873	R34294	R30740	R34293	R45658	R40843	R14372	R89278	R24863	R24862	R28304	R85092	4	3	4	5	R51083	3,	R95015	
•		Chimeric Cre-LDB-GR(I		K2 protein s	Sequence of serrapept	rificans COB	1-carboxylase.	Amino acid sequence o	lori cytopla	pancreatic lip	ricus	HPL(-) mutant with GP	rucate	rucat	ne r	in oxidase.		las	of pre-pro	ence of pre-pro	alpha-amylase	ike receptor pr	mental	(1-3)-beta-D-glucan s	ococcus biot	ynechococcus bioti	ďin	1-3)-beta-D-glucan	C. difficile toxin A	
		:-	:	:	;.	:.		:		1.22e+02									9.74e+01			6.14e+01				• .		٠.	•	

ALIGNMENTS

នន្តន្តន្តន	88888	588888	סק אל	RESULT ID W AC W AC W DT 1 DE G KW G KW G KW S OS S
glucosyltransferase in a mammal. The immune response results in reduction of the colonisation or accumulation of mutans streptococcal strains in the mammal. Compositions containing W34156 specifically interfere with the glucan-binding activity of the streptococcal glucosyltransferase. The peptides can also be used in vaccines for preventing dental caries in mammals. Sequence 22 AA;	one or more of these sequences linked to a lystne core matrix (see W34161-W34165). A composition comprising one of these sequences can be administered to a mammal to raise an immune response, in a method for interfering with the enzymatic activity of streptococcal	W34156-W34160 represent immunogenic fragments of the Streptomyces mutans glucosyltransferase (GTF) enzyme. W34157 and W34158 are from the catalytic domain of GTF, while W34160 is from the GTF surface domain. W34156 and W34159 are from the glucan-binding domain of GTF. These sequences can all be used in the immunogenic composition of the	11-NOV-1997. 01-MAY-1992; 877295. 30-APR-1993; US-057162. 30-APR-1993; US-877295. 01-MAY-1992; US-877295. (FORS-) FORSYTH DENTAL INFIRMARY FOR CHILDREN. Smith DJ, Taubman MA; WPI; 97-558089/51. Immunogenic compositions containing streptococcal glucosyl:transferase peptide(s) - used for provoking immune response to streptococcal glucosyl:transferase for preventing dental caries	HT 1 W34159; W34159; 18-FEB-1998 (first entry) 18-FEB-1998 (pry tentry) GTF antigenic peptide #4. Glucosyltransferase; GTF; enzyme; immunogen; catalytic domain; vaccine; surface domain; glucan-binding domain; mutans streptococcal strain; immune response; glucan-binding activity; dental caries prevention. Streptococcus mutans. US5686075-A.

Local

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RESULT 3

ID W34164;

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Best Local :
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11-NOV-1993; U04094.
30-APR-1993; U5-877295.
(FORS-) FORSYTH DENTAL I.
Smith DJ. Taubman MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              synthetic glucosyl-transferase peptide(s) - provoke T- and B-cell reactions in mammals, and are effective against dental caries claim 3; Page 23; 38pp; English.

The sequences (R43594-98) are subsequences from GT, they provoke T- and B-cell responses in mammals. The can be used to produce a vaccine comprising 2 of these sequences attached to a peptidyl core matrix. They are useful in producing T-cell responses to the GT enzyme causing a reduction of colonisation or accumulation of mutans steptococcal strains in mammals. The vaccines can be use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GT; glucosyltransferase; immunoresponse; peptidyl tetanus; measles; polio.
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                                                                                                                         Modified_site
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quence 22
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93-368721/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard;
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17; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 77.3%;
17; Conservative
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/note=
                                                                                                                           24
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                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.58;
77.38;
"the alpha amino acid group of Lys(24) forms a peptide linkage with the carboxyl amino group Lys(23); the omega amino group of Lys(24) form peptide bond with a second Lys residue analogo to Lys(23)"
                                                                                                                                            "Lys(23) is linked to one copy of the antigenic peptide through the alpha-amino group, and to a second copy of the peptide (not shown) via the omega amino group"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFIRMARY FOR CHILDREN
                                                                                                                                                                                                                                                                                                                                          "attached
                                                                                                                                                                                                                                                                                       GTF antigenic peptide #4 (see W34159)
'attached to the dendritic polylysine core via the alpha-amino group of Lys(23); a second copy of the antigenic 22-mer is linked to Lys(23) via the
                                                                                                                                                                                                                                                                      omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; T-cell; B-cell;
core matrix; dental cari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
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3; M
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No. 4.41e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           caries; diptheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pr jucosy:transferase peptide(s) - used for provoking immune response for streptococcal glucosy:transferase for preventing dental carles claim 12; Column -; 11pp; English.

CW 33461-734465 represent the Streptomyces mutans glycosyltransferase (GTF) CC w3461-734165 represent the Streptomyces mutans glycosyltransferase (GTF) CC enzyme immunogenic fragments shown in W34156-W34160 linked to a polylysine core. W34157 and W34158 are from the catalytic domain of GTF, while W34160 is from the GTF surface domain. W34156 and W34159 are from the glucan-binding domain of GTF. These sequences, and the immunogenic composition of the invention. A composition composition of the invention. A composition composition of the invention composition or a method for interfering with the enzymatic activity of streptococcal glucosyltransferase in a mammal. The immune response results in reduction of the colonisation or accumulation of mutans streptococcal strains in the mammal. Compositions containing W34156 specifically interfere with the streptococcal glucosyltransferase.
Query Match
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11-NOV-1997.
01-MAY-1992; 877295.
30-APR-1993; US-057162.
01-MAY-1992; US-877295.
(FORS-) FORSYTH DENTAL II
                                                                                                                                                     Claim 13; Page 15; 29pp; Japanese.

Claim 13; Page 15; 29pp; Japanese.

The DNA sequence from Streptococcus sobrinus strain 6715 encodes glucosyltransferase-I (and mutants). The DNA was obtd. by treating slucosyltransferase-I (and mutanolysin, extracting the chromosomal DNA, partially digesting with SauJAI and fractionating on agazose gel. The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109 transformed with it. A GT-1 expressing clone was isolated and sequenced. The clone may be used in the development of a drug for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GT-1; Streptococcus; de Streptococcus sobrinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-JUN-1993 (first e Glucosyltransferease
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R32925;
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25-JUL-1991; JP-186592.
                                                                                                                                                                                                                                                                                                                                                                                                                             sobrinus DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA sequence
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(KATO/) KATO K.
WPI; 93-079449/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                               dental
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1 TGARTINGQLLYFRANGVQVKG
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Similarity
17; Conser
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17; Conser
                                                                                                               1592
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72.3%;
larity 77.3%;
Conservative
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sequence with at least one
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Pred. No. 4.41e-05;
3; Mismatches 2
                          Score 112;
Pred. No. 7
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me nucleotide added or
.62e-05;
                                                          DB 6;
                                                    Length 1592;
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23-OCT 1995; U13737.
24-OCT 1994; US-329154.
16-MAR 1995; US-405496.
14-APR 1995; US-422711.
07-JUN 1995; US-482064.
(OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-AUG-1995; AU0527.
24-AUG-1994; AU-007643.
(GIFFY) GIFFARD P M.
(JACQ/) JACQUES N A.
(SIMP/) SIMPSON C L.
(GIFFAT PM, Jacques NA,
WPI; 96-151376/15.
N-PSDB; T13139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence represents an alpha-D-glucosyltransferase from Streptococcus salivarius. The enzyme is primer-independent, and produces soluble glucan from sucrose. A gene encoding the enzyme may be cloned and expressed in Escherichia coli using a subclone of phage lambda-Cl3, e.g. plasmid pGSG501 or plasmid pGSG502. The DNA may also be expressed in a transgenic plant, to improve the level of stored carbohydrate in a pasture plant which normally contains low levels, or to prevent degradation of stored carbohydrate during plant senescence. Dextran may be isolated from the plant, for use as a food binder or pharmaceutical additive. Primer independence ensures that the enzyme will be functional in plants. The glucan is poorly degraded in plants but easily degraded by bacteria in the rumen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1533 tgqqvingkqlyfdgsgrqvkg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alpha-D-glucosyltransferase.

Alpha-D-glucosyltransferase; primer-independent; soluble glucan, alpha-D-glucosyltransferase; primer-independent; soluble glucan, sucrose; transgenic plant; cloning; Escherichia coli; phage lambda-Cl3; vector; plasmid pGSG501; plasmid pGSG502; gene transfer; crop improvement; storage carbohydrate; pasture; feedstuff; senescence; dextran; binder; food; pharmaceutical. Streptococcus salivarius strain ATCC 25975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diarrhoea; diagnosis; therapy.
Clostridium difficile VPI strain 10463 (ATCC 10463).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxin
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C. difficile toxin A (aa1870-2680).
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R91047 standard;
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                                                                                    96-230603/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; cytotoxin; enterotoxin; fusion
        to form a
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13; Conser
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        s comprising anti-toxins
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59.1%;
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    protein and part of lostridium botulinum
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                                                                                                                                                        Thalley
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type A, and
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R95016 standa R95016; 08-JUL-1996

(first entry)

standard;

Protein;

2710

C. difficile toxin A.

Toxin A; cytotoxin; enterotoxin; fusion protein; ant vaccine; diarrhoea; diagnosis; therapy.

Clostridium difficile VPI strain 10463 (ATCC 10463).

fusion protein; antitoxin;

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RESULTANCE OF THE PROPERTY OF 
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A protein (R95017) comprising amino acids 1873-2684 of Clostridium difficile VPI strain 10463 toxin A (see also R95016) was obtd. by PCR amplification of genomic DNA. The PCR product can be expressed in transformed E. coli host cells as a soluble fusion protein, with maltose binding protein or a polyhistidine affinity tag as fusion partner. The resulting soluble fusion proteins, which are substantially endotoxin-free, can be used in anti-clostridial vaccines or to raise avian antibodies useful in clostridial antitoxi therapy for humans and animals.

Sequence 812 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A recombinant protein (R95014) comprises amino acids 1870-2680 of Clostridium difficile VPI strain 10463 toxin A (see also R95016), a cytotoxin associated with diarrahoetic disease. It was obtd. by PCR amplification of genomic DNA, and was expressed as a soluble fusion protein, with maltose binding protein as fusion partner, it transformed E. coll host cells. The soluble fusion protein can be used to raise arian antibodies useful as antitoxins or diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion proteins comprising non-toxin protein and part of toxin useful to form anti-toxins against Clostridium botulinum type A, C. difficile type toxins, and to treat C. difficile intoxication,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C. difficile toxin A (aal873-2684). Toxin A; cytotoxin; enterotoxin; fu immunogen; diarrhoea; diagnosis; th clostridium difficile VPI strain 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Williams JA;
WPI; 96-230603/23.
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                                                                                                                                                                                                                                                                                       588
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larity 52.2%;
Conservative
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strain 10463 (ATCC 10463).
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treat
                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                       No.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67;
                                                                                                                                                                                                                                                                                                                         DB 17; Lc...
9.21e+00;
7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1/,
9.21e+00;
9.25e 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ი
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                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thalley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clostridial antitoxin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n partner, in rotein can be r diagnostics.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Host cell containing recombinant expression vector encoding Clostridium botulinum type B or E toxin - useful to treat humans at risk of intoxication with clostridial toxin Example 15; Page 220-330; 428pp; English.

This is the amino acid sequence of Clostridium difficile toxin A, deduced from the coding region (see v90560) of the toxin A gene. Toxin A is a potent cytotoxin that plays a direct role in damaging gastrointestinal tissues. Severe cases of C. difficile intoxication result in pseudomembranous colitis. This would be prevented by neutralising the effects of toxin A in the gastrointestinal tract. Examples are provided of the production of recombinant C. difficile toxin A in host cells and of the in toxin A polypeptides. The invention specifically relates to recombinant proteins derived from Clostridium botulinum toxins (see W68389-400) and their use as immunogens for the production of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partic. diarrhoea
Claim 63; Page 290-302; 434pp; English.
Clostridium difficile VPI strain 10463 toxin A (R95016), the
product of the toxin A gene (T2928), is a potent cytotoxin that
plays a direct role in damaging gastrointestinal tissues and is
associated with diarrhoetic disease. It can be obtd. by expression in
transformed E. coli hosts of portions of DNA that together cover the
entire toxin A gene. Toxin A, and portions of it (see also
R95014-15 and R95017), pref. expressed as fusions to polyhistidine
affinity tags or maltose binding protein, are used to raise avian
antibodies useful as antitoxins or diagnostics, and in vaccine prodn.
Sequence 2710 AA;
                                                                                                                                                                                                                                                                                                                     W09808540-A1.
05-MAR-1998.
28-AUG-1997; U15394.
28-AUG-1996; US-704159.
(OPHI-) OPHIDIAN PHARM INC
Thalley BS, Williams JA;
WPI: 98-230234/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams JA;
WPI; 96-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W09612802-A1.
02-MAY-1996.
23-OCT-1995; U13737.
24-OCT-1994; US-329154.
16-MAR-1995; US-405696.
14-APR-1995; US-408604.
07-JUN-1995; US-480604.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium difficile toxin A. Antitoxin; vaccine; cytotoxin; pseudomembranous enterocolitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 9
W68387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2460 tglrtidgkkyyfntntavavtg 2482
                                                                                                                                                                                                                                                                                                                                                                                                                                         Clostridium difficile.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fusion proteins comprising useful to form anti-toxins
                         vaccines
                                                                                                                                                                                                                                                                                                         N-PSDB; V30560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; T29248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPHI-) OPHIDIAN PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     difficile type toxins, and rtic. diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Н
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96-230603/23.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
and 2710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 43.2%;
Similarity 52.2%;
12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kink JA,
                         antitoxins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein; 2710
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                                                                                                                                                                                                                                                                                                                                                           INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  non-toxin protein and part of toxin against Clostridium botulinum type A, and to treat C. difficile intoxication,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
Pred.
3; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        toxin A; intoxication; immunogen;
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. 9.21e+00;
-hos 7;
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Query Match

3

. 28 ;

Score

67;

DB 35;

Length

This sequence represents

mouse phosphotriesterase related protein

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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphottlesterase-related protein.

Phosphottlesterase-related protein, mouse; PRP; recessive cpk; murine; polycystic kidney disease; PKD; acute renal injury; autosomal dominant; autosomal recessive; fluid-filled cyst; nephron; collecting duct; kidney; renal parenchyma; renal failure; mammal; diagnostic marker; therapy; acute organophosphate toxicity; phosphotriesterase inhibitor; anti-cancer drug enhancer; anti-HIV drug collections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIT 11
W06416 standard; prot
W06416;
28-JAN-1997 (first e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  reagent; chicke Gallus gallus. W09518217-A1.
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R78621 stand
R78621;
11-JUN-1996
                                                                                                                                                                                                (UNIV ) UNIV KANSAS.

Calvet JP, Hou X, Magenheimer
WPI: 96-412067/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p-B3. P-B3 can be used as a reagent for introducing human type sugar chains onto proteins, or for the treatment of genetic disorders involving missing sugar chains. It may also be used as a tumour migration inhibitor, viral infection preventative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tsuji
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GalNAc-alpha-2,6-sialyltransferase P-B3; anti-inflammatory; viral infection; tumour; migration; inhibitor; sugar chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New GalNac-alpha-2,6-sialyl:transferases P-B1 and P-B3 - for e.g treatment of genetic disorders involving missing sugars Claim 4; Pages 52-55; 70pp; Japanese. Q95325 encodes R78621 chicken GalNac-alpha-2,6-sialyltransferase
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24-DEC-1993; JP-348260.
28-MAR-1994; JP-057369.
28-APR-1994; JP-091507.
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                                                                                                     prods.
                                                                                                                          Mouse phospho:tri:esterase-related
                                                                                                                                                                                                                                                                                                  21-NOV-1994; 343027.
21-NOV-1994; US-343027.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 95-246383/32.
N-PSDB; Q95325.
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                                  Claim 1; Column
                                                                  failure
                                                                                                                                                                       N-PSDB; T43210
                                                                                                                                                                                                                                                                                                                                                                               03-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus.
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                                                                                                     for
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Similarity 45.0%;
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                                                                                              diagnosis
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                                  25-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
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Kurosawa N,
                                                                                                 poly:cystic
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Pred. No.
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3; 1
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                               English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22
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Mismatches 7;
                                                                                              c kidney
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The mPRP sequence has abnormal underexpression in the

recessive

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IDENULT
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infections

Claim 12; Page 327; 483pp; English.

This sequence represents a Streptococcus pneumoniae protein that, based con homology with Bacteroides nodosus protein, is a peptide chain release factor 3 (RF-3), and is encoded by a DNA sequence of the invention.

CC The DNA sequences were isolated from Streptococcus pneumoniae strain CC 0100933 (NCIMB 40794). The Streptococcus pneumoniae proteins of the CC invention can be used to identify compounds which interact with and CC inhibit or activate the activity of the proteins. Antagonists can be used to treat diseases caused by S. pneumoniae proteins or through genetic cin a mammal by inoculation with the S. pneumoniae proteins or delivery CC of the encoding nucleic acids in a vector adequate to produce antibody CC and/or T cell immune responses to protect the animal from disease. The CC capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to identify antimicrobial compounds which are CC capable of inhibiting their bloactivity. In particular the proteins of the invention can be used to prevent adhesion of bacteria to mammalian cell invention of bacteria to mammalian cell invention of pathogenesis in infections initiated other than by the implantation of in-dwelling devices or other surgical techniques.

So Sequence 207 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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W38549;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Streptococcus pneumoniae diagnosing anti-microbial agent
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14-MAY-1997; U07950.
14-MAY-1996; US-017670.
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Local Similarity 53.8%;
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Pred. No. 3.04e+01;
3; Mismatches 3;
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ts for treatment of bacterial
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Query Match

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                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                            Principling meningitis and pneumonia processing processing the present sequence is Streptococcus pneumoniae peptide releasing CC The present sequence is Streptococcus pneumoniae peptide releasing CC factor (prfC). PrfC polypeptides and polynucleotides are useful for CC diagnosing susceptibility to diseases by detecting mutations or CC diagnosing susceptibility to diseases by detecting mutations or CC diagnosing diseases caused by organisms comprising the presence or CC amount of prfC polypeptide in cell or tissue samples. This method is cuseful for diagnosing the stage of infection and the type of pathogen. CC prfC polypeptides and polynucleotides can be used to screen for CC compounds), which can be used in treatment to enhance or block prfC cativity. PrfC polypeptide is useful for screening for antibacterial cc infections. PrfC polypeptides, polynucleotides and managination (gene therapy) to protect against bacterial cc infections. PrfC polypeptides, polynucleotides and antagonists may be used as a wound treatment to prevent adhesion of bacteria to matrix CC pathogen and mammalian host. PrfC antibodies are also useful for inducing an immune response to immunise and prevent disease, and for isolating CC diagnosed, prevented or treated include: othis media, conjunctivitis, cc especially meningitis.

Sequence 514 AA;
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W03642;
17-DEC-1996
17-DEC-1996 (first entry)
Human cannabinoid GPR N-terminal sequence.
G-protein coupled receptor; ligand binding assay; transmembrane domain schizophrenia; dopamine; cAMP; adenosine; thrombin; adrenergic; opsin; muscarinic acetylcholine; endothelin; bombesin; endocrine; rhodopsin;
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W83359
W83359;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Streptococcus pneumoniae peptide releasing factor polypeptide and polynucleotide - useful as diagnostic reagents and for prevention and treatment of diseases caused by bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus pneumoniae prfC protein sequence. Streptococcus pneumoniae; prfC; antibacterial; meningitis; pneumonia; peptide releasing factor; otitis media; conjunctivitis; bacteremia; sinusitis; pleural empyema; endocarditis; immunisation; infection;
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29-MAY-1997; US-865311
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WPI; 99-00
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Pred. No. 3.
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PT for treating schizophrenia

PS Disclosure; Fig 8B(3); 184pp; English.

CC Proteins W02657-W02720 represent a range of G-protein coupled receptor

CC (GPR) proteins selected from cAMP, adenosine, muscarinic acetylcholine,

CC adrenergic, thrombin, endothelin, bombesin, endocrine, rhodopsin, opsin,

CC odorant, cytomegaloviral and other GPR proteins. The peptides

CC W03578-W03651 represent the N-terminal fragments of the above proteins.

The receptor proteins were used to design polypeptides, pref. based on

the transmembrane domains, for use in G-protein coupled receptor ligand

CC binding assays. The polypeptide fragments retain biological activity

CC such as binding a GPR ligand or modulating GPR ligand binding to a GPR

CC (see W02747-W02999 for examples of polypeptide fragments).

CC The polypeptide fragments can be used in compositions for treating

CC subjects suffering from a pathology related to a GPR abnormality e.g. a

SQ Sequence 116 AA;
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10-SEP-1996.
10-SEP-1992; 943236.
10-SEP-1992; US-943236.
09-SEP-1993; US-118270.
4 (UNNY) UNIV NEW YORK STATE.
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Best Local Similarity 50.0%;
Matches 8; Conservative
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Best Local
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US7564075-A.
US7564075-A.
03-SEP-1991.
08-AUG-1990; US-564075.
08-AUG-1990; US-564075.
(USSH ) NAT INST OF HEALTH.
Matsuda L, Brownstein M, Bonn
WPI; 91-30326/41.
N-PSDB; Q14003.
                                                                                                                                                                                      DNA encoding mammalian cannabinoid receptor - used for producing receptor for screening drugs and ligands and in detection Disclosure; Fig 5; 25pp; English.

SKR6 cDNA encoding the rat cannabinoid receptor was isolated from a rat cerebral cortex cDNA library. An EcoRI-XbaI fragment was used to screen a human cosmid library. A positive clone was identified and sequenced. There is ca. 97 per cent homology between this amino acid sequence deduced from the sequence of the positive human clone and rat cannabinoid receptor (see R14195). Recombinantly produced receptor can be used to screen for new drugs suitable for treatment of cannabinoid-treatable conditions, e.g. glaucoma, bronchial asthma,
                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human cannabinoid receptor.
Cannabis sativa; marijuana; drug test; substance K receptor.
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R14196 standard; Protein; 472 AA.
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Local Similarity 50.0%;
hes 8; Conservative
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                                                                                                                                                            472 AA;
                                                                           Score 60; DB 3; L
Pred. No. 4.87e+01;
3; Mismatches 5
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Pred. No. 4.87e+01;
3; Mismatches 5;
                                                                                                                 Length 472;
                                                                               5; Indels
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Search completed: Tue Jan 11 15:46:47 2000 Job time : 19 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: lar output not generated. Tue Jan 11 15:49:24 2000; MasPar time 1.77 Seconds 147.986 Million cell updates/sec

Description:
Perfect Score:
Sequence: Scoring table: PAM 150 Gap 15 1 TGARTINGQLLYFRANGVQVKG 22 >US-09-290-049-3 (1-22) from US09290049.pep

Title:

Searched: 122461 seqs, 11912985 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 19.644; Variance 62.865; scale 0.312

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Score Match Length DB ID Description 114 73.5 22 1 US-08-057 Sequence 3, 67 43.2 811 2 US-08-405 Sequence 7, 67 43.2 811 1 US-08-480 Sequence 7, 67 43.2 811 1 US-08-480 Sequence 6, 67 43.2 2710 2 US-08-480 Sequence 6, 67 43.2 2710 1 US-08-480 Sequence 6, 63 40.6 40.7 US-08-666 Sequence 1, 62 40.0 349 1 US-08-480 Sequence 1, 62 40.0 349 1 US-08-480 Sequence 1, 62 40.0 349 1 US-08-480 Sequence 2, 59 38.1 91 2 US-08-480 Sequence 8, 59 38.1 453 2 US-08-485 Sequence 6, 59 38.1 453 2 US-08-485 Sequence 6, 59 38.1 453 2 US-08-476 Sequence 6, 59 38.1 453 2 US-08-476 Sequence 6, 59 38.1 453 1 US-07-956 Sequence 6, 59 38.1 453 1 US-07-956 Sequence 2, 59 38.1 453 1 US-07-956 Sequence 2, 59 38.1 453 1 US-08-476 Sequence 2, 59 38.1 453 1 US-07-956 Sequence 2, 59 38.1 453 1 US-08-956 Sequ	Result
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Sequence 25	Sequence 19	Sequence 19	Sequence 19	Sequence 19	Sequence 19	Sequence 3,	Sequence 3,			Sequence 2,	Sequence 2,	Sequence 2,	Sequence 23	Sequence 9,	Patent No.	Sequence 2,	Sequence 2,	Sequence 2,	Patent No.	Sequence 4,	Sequence 4,
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TIPE: amino acid STRANDEDNESS: single	:	Transcream	APPOTENCE CURRENT CATOR.	;		TELEPHONE: (617) 861-6240	ö		REGISTRATION NUMBER: 34,480	NAME: Wagner, Richard W.	ATTORNEY/AGENT INFORMATION:	FILING DATE: 01-MAY-1992	Z		CLASSIFICATION: 424		≉	TA:	PatentI	SYSTEM:	COMPUTER: IBM PC compatible	MEDIUM TYPE: Floppy disk	COMPUTER READABLE FORM:	Ξ.	∺	••	Lexington	o Militia Drive	ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.	Ñ	SEQUENCES: 5	VENTION	Smith, Daniel J.	APPLICANT: Taubman Martin A	GENERAL INFORMATION:	5686075	Sequence 3, Application US/08057162B	,	Sequence 3, Application US/08057162B			XXXXXX		LT 1 US-08-057-162B-3 STANDARD; PRT; 22 AA.

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Best Local Similarity 77.3%;
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SEQUENCE 23
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 SEQUENCE
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                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/161,907

FILING DATE: 02-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION UNUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION UNMBER: US 07/429,791

FILING DATE: 31-CCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: INGOLIA, DIANE E.

NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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APPLICANT: WILLIA
                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                        REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
                                                                                                                                                                                                                                                                             FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/405,499
                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: VACCINE FOR CLOSTRIDIUM BOTULINUM TITLE OF INVENTION: NEUROTOXIN
             MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polaris
                    TYPE: amino acid
STRANDEDNESS: un)
TOPOLOGY: unknown
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o. 5919665
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22 AA; 2366 MW;
811 AA; 91921 MW; 3356332 CN;
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                      unknown
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             protein
                                   unknown
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Pred. No. 2.93e-05;
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                                        APPLICATION NUMBER: US 07/429,791
FILLING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INFOLIA, DIAME E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                    TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                 FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/00
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0: FILING DATE: 14-APR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL, LLP
STREET: 220 MONTGOMERY STREET, S
            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                      FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
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APPLICATION NUMBER:
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larity 52.2%;
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811 amino acids
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TELECOMMUNICATION INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION UMBER: US 08/405,496
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/480,604;
FILING DATE: 07-UN-1995
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CITY: SAN FRANCISCO
CITY: CALIFORNIA
STATE: CALIFORNIA
THATTED STAT
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TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KINK, JOHN A.
APPLICANT: THALLEY, BRUCE S
APPLICANT: PADHYE, NISHA V.
APPLICANT: FIRCA, JOSEPH R.
                                     FILING DATE: 31-OCT-1989 ATTORNEY/AGENT INFORMATION:
                                                                         APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                   PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                               APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 94104
                                                               APPLICATION NUMBER:
            REGISTRATION NUMBER:
                           NAME:
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811 AA; 91921 MW; 3356332
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                         INGOLIA, DIANE E.
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220 MONTGOMERY STREE
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                                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES
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                                                    JMBER: US 07/429,791
31-OCT-1989
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NUMBER:
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           40,027
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Pred. No. 5.11e+00;
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STREET, SUITE 2200
OPHD-01763
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Best Local S
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PRIOR APPLICATION UNMBER: US 07/429,791
FILING DATE: 31-0CT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIAME E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: 0PHD-01308
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAY: (415) 397-8338
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-405-496A-6
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 25-OCT-PRIOR APPLICATION DATA:
                                                                                                                                                                                             CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
US 08/329,154
                                                                                                                        APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
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JENCE 812 AA; 92022 MW; 3364670
                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 3
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FILING DATE: 16-MAR-1995
CLASSIFICATION: 424
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TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                          ZIP: 94104
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Similarity 52.2%;
12; Conservative
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220 MONTGOMERY STREET, SUITE 2200
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                                                                                                                                                                                        25-OCT-1994
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                                         40,027
ER: OPHD-01308
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Pred. No. 5.11e+00;
3; Mismatches 7;
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Best Local S
Matches 1
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Patent No. 5736139
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Local Similarity 52.28;
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                                   APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NUMBER: TIMES TIMES TIMES TO THE TIMES TO T
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APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN 6
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JENCE 2710 AA; 308053 MW; 38468929 CN;
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LENGTH: 2710 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: STAFFORD, DOUGLAS C.
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
TITLE OF INVENTION: PREVENTION OF C. DIFFICILE DISEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                           FILING DATE: 02-DEC-1993 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
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Pred. No. 5.11e+00;
Viamatches 7; Indels
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 SEQUENCE
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                             INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 404 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application Patent No. 5854042
                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGARTINGOLLYFRAN-GVOVKG 22
                                                                                                                                                                                                                                                                                              ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                   OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Shuichi TSUJI et al.
TITLE OF INVENTION: NOVEL SUGAR-CHAIN SYNTHETASE AND PROCESS FOR
TITLE OF INVENTION: PRODUCING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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LENGTH: 2710 amino aci
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                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J
REGISTRATION NUMBER: 33,
                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                     ORIGINAL SOURCE:
                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                TELEX:
                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: August
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                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
ORGANISM: G. gallus (chicken)
CE 404 AA; 45826 MW; 844143 CN;
                                                                                                            TELEFAX:
                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: protein 2710 AA; 308053 MW; 38468929 CN;
                                                                                                                                                                                                                                                                                                                                                   Washington
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ilarity 52.2%;
Conservative
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805 Fifteenth Street, N.W.,
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                                                                                                                                                                                                                                                                                    IBM Compatible
                                                                                                                                                                                                                              August 19,
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                                                                                                                                                                                                                                 US/08/666,367B
: 19, 1996
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Pred. No. 5.11e+00
                                                                                                                                                     33,367
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Best Local Similarity 45.0%;
                                                                                                                                                    Query Match
Best Local
                                                                                                                           Matches
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08343027A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5552313
GENERAL INFORMATION:
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                                                                          79 AIREELLYFKAYG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 349
                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adler, Dr. Benjamin A.
NEGISTRATION NUMBER: 35,423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft Word for Macintosh CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,027A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: Protein HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                   ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Calvet, James P., TITLE OF INVENTION: DNA Enco
                    TINGQLLYFRANG 17
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DEVELOPMENTAL STAGE:
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OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: UZIP: 77071
                                                                                                                                                                                                                                                                                                 TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
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                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
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                                                                                                                                               Similarity
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                                                                                                                                                                                                                       LINE: 349 AA; 39253 MW; 609827 CN;
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8011 Candle Lane
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                                                                                                                   Score 62; DB 1; Length 349;
Pred. No. 1.67e+01;
3; Mismatches 3; Indels
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Pred. No. 1.32e+01;
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e Phosphotriesterase-Related Protein
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Best Local Similarity
Matches 8; Conser
Sequence
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                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows 95
OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/865,311
FILING DATE: 29-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08865311 Patent No. 5919664
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ZIP: 19103-2793
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Falk, Stephen T
REGISTRATION NUMBER: 36,795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                             LENGTH: 514 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
NCE 514 AA; 58470 MW; 1375700 CN;
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8, Application US/08480604A
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4000 Bell Atlantic Tower, 1717 Arch
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Pred. No. 2.11e+01;
1; Mismatches 4
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Sequence 8, Application US/08480604A Patent No. 5736139 GENERAL INFORMATION:

APPLICANT:

KINK, JOHN A.

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RESULT
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Best Local
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XXXXXX
                              US-08-405-496A-8
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Local Similarity 46.7%;
hes 7; Conservative
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                                                                                                                                    3 KIINGKHFYFNNDGV 17
                                                                                                                                                                                                                                       TOPOLOGY: unknown
MOLECULE TYPE: protein
JENCE 91 AA; 10432 MW; 39683 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR AFFILION NUMBER: US UB/407,*** FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/329,154
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ADDRESSEE: MEDLEN & CARROLL, L.
STREET: 220 MONTGOMERY STREET,
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
TYPE: amino acid
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APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-0C7-1989
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
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APPLICATION NUMBER: US/08/480,604A
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                    RTINGQLLYFRANGV 18
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 04-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: INGOLIA, DIANE E REGISTRATION NUMBER: 4(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993
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04-DEC-1992
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                                                                                                                                                                                                                                                                                             unknown
                              STANDARD;
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                                                                                                                                                                   Score 59; DB 1;
Pred. No. 3.36e+01
3; Mismatches
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Best Local S
Matches
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MOLECULE TYPE: protein
SEQUENCE 91 AA; 10432 MW;
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                             Sequence 6, Application US/08485607
                                                                      XXXXXX
                                                                                          US-08-485-607-6
Sequence 6, Application US/08485607 Patent No. 5792627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08405496A Patent No. 5919665
                                                                                                                                                                                                                                                                                         TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                         Match 38.1%;
Local Similarity 46.7%;
es 7; Conservative
                                                                                                                                   4 RTINGQLLYFRANGV 18
                                                                                                                                                       3 KIINGKHFYFNNDGV 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94104
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 0 FILING DATE: 25-OCT-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPTELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 16 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentl
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/161,907 FILING DATE: 02-DEC-1993
                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CALIFORNIA
                                                                                                                                                                                                                                                                    91 amino acids
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER: US 07/985,321
04-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/405,496A
16-MAR-1995
                                                                                          STANDARD;
                                                                                                                                                                                                                                                 unknown
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                                                                                                                                                                                                                                                                                                                                                                                     US 07/429,791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US 08/329,154
                                                                                                                                                                         Score 59;
Pred. No.
3; Misma
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                                                                                          PRT;
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Query Match
Best Local Similarity
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                                                                                                                                                                         Sequence 8, Patent No.
                                                                                                                                                                                                                                                                                                                                                                       315 RIAOGEALRFROADIQLRG 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 1-312-755-448
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/956
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 579262
REGISTRATION NUMBER: 33,86
REFERENCE/DOCKET NUMBER: A
                                                                                                                                                                                                                                                                                                                                               4 RTINGQLLYFRANGVQVKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,607
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: L
MOLECULE TYPE:
                                                                              NUMBER OF SEQUENCES: 3
                                                                                                          APPLICANT: Gornicki, Piotr
TITLE OF INVENTION: ACETYL-COA CARB
TITLE OF INVENTION: METHODS FOR USE
                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Cyanobacter:
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                                 STATE:
                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino acid
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                                                        ADDRESSEE: Arnold, STREET: P.O. Box 4
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                    COUNTRY:
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                                                                                                                                                                            8, Application US/08422560A
5. 5910626
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453 AA; 49608 MW; 983857 CN;
                              Houston: TX
      77210-4433
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321 No. 5792627th Clark Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                453 amino acids
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1-312-755-4489
                                                                                                                                              Haselkorn, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linear
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SYSTEM: PC-DOS/MS-DOS
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                                                        Box 4433
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                                                                                                                     ACETYL-COA CARBOXYLASE COMPOSITIONS AND
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                                                                    White & Durkee
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Pred. No. 3.36e+01;
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Best Local Similarity 36.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 RIAQGEALRFRQADIQLRG
                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/08476537 Patent No. 5756290
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/956,700
FILING DATE: 10/21/92
ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5756290thrup
                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 8:
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                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
COMPUTER: PC DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
                                                                                                                                                                                             STREET: STREET: Chicago
CITY: Chicago
Time: Illinois
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LENGTH: 453 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 02-OCT-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 512-418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/956,700 FILING DATE: 02-OCT-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Wilson, Mark B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OGY: linear
453 AA; 49662 MW; 983072 CN;
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                                                                                                                                                                                                                                   E: Arnold, White & Durkee
321 No. 5756290th Clark Street
                                                                                                                                                                                                                                                                                                 Robert Haselkorn and Piotr Gornicki
VENTION: Cyanobacterial and Plant Acetyl-Coa
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Pred. No. 3.36e+01
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REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: AR
TELECOMMUNICATION INFORMATION:

ARCD: 058

TELEPHONE:

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Best Local Similarity 36.8%;
Matches 7; Conservative
Query Match
Best Local Similarity
                                                                                                TELEFAX: 1-314...
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
TENGTH: 453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LT 15
US-07-956-700B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXX
                                           MOLECULE TYPE: SEQUENCE 453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 6, Application US/07956700B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Application US/07956700B Patent No. 5539092
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/956,700B
FILING DATE: 19921002
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: Peptide
UENCE 453 AA; 49608 MW; 983857 CN;
                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 1-312-744-0090
TELEFAX: 1-312-755-4489
                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Thomas E. No. 5539092thrup
REGISTRATION NUMBER: 33,268
REFERENCE/DOCKET NUMBER: ARCD:058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Cyanobacterial and Plant Acetyl-CoaTITLE OF INVENTION: Carboxylase
                                                                  LENGTH: 453 amino acid
TYPE: Amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 321 NO. CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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321 No. 5539092th Clark Street
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                                         Peptide
49608 MW; 983857 CN;
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Score 59; DB 1; Length 453; Pred. No. 3.36e+01;
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Pred. No. 3.36e+01;
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               315 RIAQGEALRFRQADIQLRG 333
4 RTINGQLLYFRANGVQVKG 22
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Search completed: Tue Jan 11 15:49:31 2000 Job time: 7 secs.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: ar output not generated. Tue Jan 11 15:41:17 2000; MasPar time 3.90 Seconds 109.105 Million cell updates/sec

Title:

Sequence: Description: Perfect Score: >US-09-290-049-2 (1-20) from US09290049.pep 135 1 VPSYSFIRTAHDSEVQDLIA 20

Scoring table: PAM 150 Gap 15

Searched: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

a-geneseq35
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
24:part24 25:part25 26:part26 27:part27 28:part28
29:part29 30:part30 31:part31 32:part32 33:part33
34:part34 35:part35 36:part36 37:part37 38:part38
39:part39

Mean 20.274; Variance 61.611; scale 0.329

Statistics:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Length	DB	ID	Description	Pred. No.
_	97	71.9	1592	6	R32925	Glucosyltransferease	2.44e-03
2	71	52.6	1577	16	R91047	Alpha-D-glucosyltrans	2.33e+00
ω	63	46.7	825	4	R22237	Sequence of the "qB"	1.71e+01
4	63	46.7	873	14	R79459	aryn	1.71e+01
5	61	45.2	344	30	W52812	Human induced tumour	2.77e+01
0	61	45.2	579	16	R86406	Human matrix metallop	2.77e+01
7	61		582	16	R86407	Human matrix metallop	2.77e+01
&	61	45.2	582	14	R75648		2.77e+01
9	60	44.4	146	σ	R32010	Rp15-TIA-1.	3.53e+01
10	60	44.4	146	w	R12539	Cytotoxic T Lymphocyt	3.53e+01
11	60	44.4	156	œ	R40840	Glioblastoma derivied	3.53e+01
12	60	44.4	375	σ	R32011	TIAR.	3.53e+01
13	60	44.4	375	σ	R32009	Rp40-TIA-1.	3.53e+01
14	. 60	44.4	465	31	W54351	Vimentin.	3.53e+01
15	59	43.7	557	24	W24096	Enzyme for production	4.48e+01
16	58	43.0	159	10	R53249	Fasciola hepatica cat	5.69e+01

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548 vpsysfar-ahdsevqdii 565 ||||||| ||||||||| 1 vpsysfirtahdsevQdLI 19

RESULT 2 ID R91047 standard; Protein; 1577 AA.

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Query Matc Best Local Matches	Claim 1 The DNZ glucosy S. sobs partial The 3-5 transfc sequenc dental Sequenc	28-JUN-1993 (first ent) Glucosyltransferease I. Glucosyltransferease I. GT-1; Streptococcus; den Streptococcus sobrinus. J05023188-A. Q-FEB-1993; 25-JUL-1991; JP-186592. 25-JUL-1991; JP-186592. 25-JUL-1991; JP-186592. (FUKU/) FUKUI I. (KATO/) KATO K. WPI; 93-079449/10. N-PSDB; Q37760. DNA sequence glucosyl:tl sobrinus DNA sequence w. deleted	SULT 1 R32925		110 110 110 110 110 110 110 110 110 110
	Claim 13; Page 15; 29pp; J The DNA sequence from Stre glucosyltransferase-I (and S. sobrinus 6715 with muta partially digesting with S The 3-5 kbp fragment was I transformed with it. A GT sequenced. The clone may dental caries. Sequence 1592 AA;	N-193 Strep	1 25 star		**************************************
similarity 16; Conser	Page 1: equence cansfer: is 6715 digest: pp fragi pd with The case ites.	nnsferrotococococococococococococococococococ	dard;		3 3 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5
	from ase-I with Ing with ing with it. it. aha,	rst en ease I cus; du orinus 192. [86592]].	Protein;		1010 1014 326 792 1002 1002 1002 1003 1003 1003 1003 100
11.98; 14.28; tive	29pp; Japar omn Streptoco omn Streptoco -I (and mut th mutanoly) with Sau3# t was ligat t was ligat t was pe u	entry) I. dental; us. 92. 1:transf	in; 1		33 33 33 33 33 33 33 33 33 33 33 33 34 37 37 37 37 37 37 37 37 37 37 37 37 37
Score 97; DI Pred. No. 2.4 1; Mismatch	lese. coccus coccus cants) rsin, rsi	l; caries. sferase-I -	1592 AA.	ALIGNMENTS	R91823 W61232 W68474 R57080 R5502 R5502 R6417993 P818661 R080661 R081175 R64175 R64176
DB 6; Leng 2.44e-03; atches 1;	brinus stra The DNA was racting the actionatine pUC18 and pucked a	comprises Str			Human immunodeficienc Streptococcus pneumon HIV-1 strain YBF30 po Fasciola hepatica catt X-proly1-dipeptidy1-a HIV isolate LAV.MAL p Sequence encoded by L HIV-1 pol protein of CarR gene product. Carbapenem R. Carbapenem R. S. thermophilus exopol s. thermophilus exopol Rinder-pest virus nuc Rabbit membrane-type Carrot reverse transc Human semaphorin. KSHV glycoprotein B. Human pil0.
gth 1592; Indels	6715 btd. hrome n aga coli solat	added added			immunodeficienc tococcus pneumon strain YBF30 po ola hepatica cat tly1-dipeptidy1-a solate LAV_MAL p nce encoded by L pol protein of gene product. penem R. penem R. rest virus nuc t membrane-type t reverse transc semaphorin. glycoprotein B. pl10. s 3-kinase 110 k thetical protei nding random pep secreted protei xin 69D1. xin 69D1. xin 69D1. yP4, rotein contained ine/threonine pr
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The sequence represents an alpha-D-glucosyltransferase from Streptococcus salivarius. The enzyme is primer-independent, and produces soluble glucan from sucrose. A gene encoding the enzyme may be cloned and expressed in Escherichia coli using a subclone of phage lambda-Cl3, e.g. plasmid pGSG501 or plasmid pGSG502. The DNA may also be expressed in a transgenic plant, to improve the clovel of stored carbohydrate in a pasture plant which normally contains low levels, or to prevent degradation of stored carbohydrate during plant senescence. Dextran may be isolated from the plant, for use as a food binder or pharmaceutical additive. Primer independence ensures that the enzyme will be functional in plants. The glucan is poorly degraded in plants but easily degraded by bacteria in the rumen
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24-AUG-1994; AU-007643.
(GIFF/) GIFFARD P M.
(JACQ/) JACQUES N A.
(SIMP/) SIMPSON C L.
                        Vaccines against ILTV for use in chic
non-infectious sub-units or live reco
administered by aerosol
Example; Fig 11; 122pp; English.
The inventors claim a non-infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R22237 standard;
R22237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alpha-D-glucosyltransferase; primer-independent; soluble glucan; sucrose; transgenic plant; cloning; Escherichia coli; phage lambda-Cl3; vector; plasmid pGSG501; plasmid pGSG502; gene transfer; crop improvement; storage carbohydrate; pasture; feedstuff; senescence; dextran; binder; food; pharmaceutical. Streptococcus salivarius strain ATCC 25975.
                                                                                                                                                                                                                                     23-AUG-1991; AU0383.
24-AUG-1990; AU-001937.
(WEBS-) WEBSTER A PTY LTD.
Sheppard MG, Prideaux C, J
                                                                                                                                                               WPI; 92-096898/12.
N-PSDB; Q22989.
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05-MAR-1992.
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Sequence of the "gB" homol
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Alpha-D-glucosyltransferase.
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96-151376/15.
          which
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Similarity 57.9%;
11; Conservative
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1577 AA;
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     of ILTV.
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22-AUG-1995
29-OCT-1991; 788123.
29-OCT-1991; US-788123.
19-NOV-1993; US-156866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R79459;
                 Human induced tumour melanoma; carcinoma. Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acids can be used as probes, for antisense control of gB gene expression or for production of gB polypeptides. The gB polypeptides can be used for the production of antibodies (both used in immunoassays) and in vaccines. Recombinant avipox virus expressing the ILV gB can be used for immunising fowl, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Infectious Laryngotracheitis virus gB glycoprotein.
Infectious Laryngotracheitis virus; gB; glycoprotein; antibody; vaccine; immunoassay; detection; identification; avipox; chicken;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene.
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                                                                                                                                            W52812 standard; Protein; W52812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expressing chickens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 95-302091/39.
N-PSDB; Q97351.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYDE ) UNIV DELAWARE. Keeler CL, Poulsen DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fowl; probe; antisense; gene expression.
Gallid Herpesvirus 1.
                                                                                            Human induced
                                                                                                                     07-JUL-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated Infectious Laryngotracheitis Virus gB gene - develop prods. for detection and for vaccine(s), part:
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claim 1; Columns 11-16; 11pp;
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decoded polypeptide
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Pred. No.
7; Misma
                                                                                                                                                                                                                                                                                                                                                                 Pred.
7; 1
                                                                                                                                                                                                                                                                                                                                                                                                                 Score
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                                                                      HITP;
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     63; DB 14;
No. 1.71e+01
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••
                                                                   prevention;
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                                                                      cancer;
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21-SEP-1995.
17-MAR-1995; D00357.
17-MAR-1994; DE-409663.
21-OCT-1994; DE-438838.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997; U14378.
16-AUG-1996; US-689974.
(INCY-) INCYTE PHARM INC.
Au-Young J, Hawkins PR;
WPI; 98-159538/14.
                                                           New matrix metallo:protease(s) and DNA encoding them - also vectors, recombinant cells and complexes with ligands, useful as proteolytic agents and for identification of specific inhibitors and activators claim 8: page 30; 85pp; German.

The present sequence is that of human matrix metalloprotease MMPmla. The protein has mol. wt. 65591 and comprises a signal peptide, pro-region, conserved catalytic domain and haemopexinhomologous sequence, all typical of known metalloproteases. MMPmla differs from known metalloproteases in having a hydrophobic region near the C-terminus, suggesting that the protein is membrane-bound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig 1; 61pp; English.
Claim 1; Fig 1; 61pp; English.
The present sequence is human induced tumour protein (HITP), which can be used to treat and prevent cancer, specifically melanoma and carcinoma of the breast, colon or brain. HITP 1 cancer cell differentiation, and stops cell division.
                                                                                                                                                                                                                      Hinzmann B, Will I
WPI; 95-336975/43.
                                                                                                                                                                                                                                                                                                                                                                                              domain
                                                                                                                                                                                                                                                                                                                                                                                                                       region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; matrix metalloprotease; activator; zinc-binding region.
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19-FEB-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc_difference
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human matrix metalloprotease MMPmla.
              antibodies.
                        detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ry Match
                          MMP proteins can hydrolyse extracellular matrix proteins and are involved in certain pathologies. The new MMP will be useful for letecting MMP inhibitors or activators and to generate diagnostic
                                                                                                                                                                                                                                    (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour induced protein and related formed cells and antibodies, useful rentiation of cancer cells, and for
579
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/note=_"contains 3
                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "conserved region within pro-sequence,
contains a Cys residue"
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4; N
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                                                                                                                                                                                                                                                                                                                                                                 His residues
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2.77e+01;
--heg 3;
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Best Local Similarity
Matches 5; Consei
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Best Local
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R75648;
R75648;
31-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; Page 30-31; 85pp; German.

The present sequence is that of human matrix metalloprotease MMPmlb. The protein has mol. wt. 65900 and comprises a signal peptide, pro region, conserved catalytic domain and haemopexin-homologous sequence, all typical of known metalloproteases. MMPmlb differs from known metalloproteases in having a hydrophobic region near the C-terminus, suggesting that the protein is membrane-bound. MMP proteins can hydrolyse extracellular matrix proteins and are involved in certain pathologies. The new MMP will be useful for
  Homo
Key
cds
                                                                  Human placenta derived metalloprotease. Human placenta; metalloprotease; probe; monoclonal antibody; cancer; treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New matrix metallo:protease(s) and DNA encoding them recombinant cells and complexes with ligands, useful agents and for identification of specific inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human matrix metalloprotease MMPmlb Human; matrix metalloprotease; MMP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R86407 standard; Protein; 582 R86407;
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21-OCT-1994; DE-438838.
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17-MAR-1995; D00357.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DELB-) DELBRUECK CENT Hinzmann B, Will H; WFI; 95-336975/43.
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                                                                                                                                                                                                                                                                                163 pyayireghekqadimi 179
:|::|| :|: : :|
3 SYSFIRTAHDSEVQDLI 19
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:|::|| :|: : :|
                                              sapiens.
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                                                                                                                                                                                       standard; Protein; 582
                                                                                                                                                                                                                                                                                                                                                                             Similarity 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MMP inhibitors
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                                                                                                                                         (first entry)
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239..2
  Location/Qualifiers 112..1860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "conserved region
contains a Cys residue"
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Pred. No. 2.77e+01;
8; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                             Score 61; DB 16;
Pred. No. 2.77e+01;
8; Mismatches 4
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                                                                                             detection;
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s proteolytic
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Best Local S
Matches
                                                                                                                                                                                                                                             processes high levels of TIA-1 antigen was used for theconstruction of a cDNA library in lambda gtil. When this expression library was screened using TIA-1 monoclonal antibody, several bacteriophage expressing immunoreactive fusion proteins were identified. Cross hybridisation analysis cluster three independent clones contg. related cDNAs. The largest cDNA insert was used to probe the original library for largest cDNA insert was used to probe the original library for antigen. The antigen is active in lymphocyte-mediated cytotoxicity and can eliminate a wide variety of virus infected or transformed target cells. TIAR or TIA-1 antigen may be linked chemically or recombinantly to cell targetting ligands such as growth factors, hormone or antibodies, and may be used to kill targetted cells, e.g.
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30-NOV-1994; J02009.
30-NOV-1993; JP-341061.
(FUJY ) FUJI YAKUHIN KOGYO KK.
Sato H, Seiki M, Shinagawa A;
WPI; 95-215255/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-1993. U05117. 12-JUN-1992; U05117. 10-JUL-1991; US-726607. 19-FEB-1992; US-843949.
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st Local Similarity
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R32010;
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WO9301314-A.
                                                                                                                                                                                                        Sequence
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                                                                                                44.48;
larity 31.68;
Conservative
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F, Streuli
                                                                                                Score 60;
Pred. No.
8; Misma
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Pred. No. 2.
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) applicable for cancer
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3.53e+01;
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2.77e+01;
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Best Local S
Matches
Query Match
Best Local S
Matches
                                                                                                                                                   New polypeptide from glioblastoma cell line - useful in treatment of abnormal glial cells or neurons or for treating tumours Claims 1-4; Page 14-15; 21pp; English.

Colaims 1-4; Page 14-15; 21pp; 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-MAR-1993; 301571.
03-MAR-1992; JP-081557.
22-APR-1992; JP-129558.
(ONOY) ONO PHARM CO LTD.
Konishi M, Miyamoto T, N;
WPI; 93-282254/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R40840 stand
R40840;
01-MAR-1994
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31-DEC-1990;
05-JAN-1990;
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This sequence corresponds to a 15kD immunogenic protein associated with cytoplasmic granules in cytolytic T lymphocytes and natural killer cells. The protein is found principally in a subpopulation CD8+ T lymphocytes from peripheral blood mononuclear cells. It reacts with monoclonal antibody TIA-1 (HB 10319).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anderson PJ, Streu WPI; 91-202096/28.
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Cytotoxic T Lymphocyte-specific antigen.
CTL; natural killer cells; CD8; peripheral blood; TIA-1; immunogen
                                                                                                                                Sequence 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuron; immunity; tumour; aplasia.
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(DANA-) DANA FARBER CANCER.
Anderson PJ, Streuli M, Sci
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   44.48;
larity 42.98;
Conservative
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larity 31.68;
Conservative
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derivied polypeptide.
; differentiation; pro
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cytolytic T lymphocytes and natural
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ne 60; DB 8; I
1. No. 3.53e+01;
Mismatches
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3.53e+01;
                                                              Length 156;
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CS outhern blots of genomic DNA probed with a TIA-1 antigen specific probe were unexpectedly complex suggesting that either the TIA-1 cantigen gene was very large, or that TIA-1 antigen-related genes consider the derived from PHA-activated T cells was screened with a TIA-1 antigen CC CDNA probe. Several TIA-1- related CDNAs were identified in this manner. A comparison of these varient clones with TIA-1 genomic sequences indicated that all but one were likely to be splice varients of the CC TIA-1 gene. Like TIA-1 antigen, TIAR is a member of a family of CC RNA-binding proteins, possessing 3 RNA-binding domains and a carboxy terminal auxilary domain. A segment of the CDNA is useful as a probe correct of determining the presence of cytolytic lymphocytes in a biological confective agent, e.g. HIV virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 44.48;
Best Local Similarity 31.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                              12-JAN-13-7.
12-JUN-1992; U05117.
10-JUL-1991; US-726607.
19-FEB-1992; US-843949.
(DAND ) DANA FARBER CANCER INST INC.
(DAND ) DANA FARBER CANCER INST INC.
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R32009;
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N-PSDB; Q34556.
                                                                                    N-PSDB; Q34554.
DNA encoding TIA-1 antigen
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WO9301314-A.
                                                                                                                                                                                                                                                                                                                                                                                             Rp40-TIA-1.
40 kD antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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10-JUL-1991; US-726607.
19-FEB-1992; US-843949.
(DAND ) DANA FARBER CANCER INST INC.
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                                treatment
                                                             killing of cytolytic
                                                                                                                                           Anderson PJ, Schl.
WPI; 93-045515/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 375
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  Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                             cytolytic lymphocyte; infection; HIV; targetting
35; 61pp; English
                                                          lymphocyte(s)
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    used for detecting and cytotoxic 
ocyte(s) applicable for cancer

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Pred. No. :
9; Mismai
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D W24096 standard; Protein; ...

D W24096;

T 20-NOV-1997 (first entry)

DE Enzyme for production of catechol or pyrogalol compounds.

KW Catalysis; enzyme; methyl group; vanillic acid; syringa; procatechol; pyrogarol; Pseudomonas paucimobilis.

T resudomonas paucimobilis SYK-6.
                                                                  RESULT
ID WI
AC WI
DT 2C
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KW CE
OS PS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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05-SEP-1997; G02394.
08-APR-1997; GB-007132.
06-SEP-1996; GB-018600.
(CLIN-) CENT CLINICAL & BASIC RI
BYIJalsen I, Fey SJ, Larsen P;
WPI: 98-207057718.
                                                                                                                                                                                                                                                                                                                                                                                                  Biochemical markers of human endometrium - useful for, e.g. diagnosis of hyperplasia and adenocarcinoma Disclosure; Page 20; 77pp; English.

Proteins W5349-W54364 are examples of proteins produced in the endometrium during the hyperplasia, adenocarcinoma or proliferative phase of the endometrium. The presence and quantities of these proteins can be detected using 2D gel electrophoresis comparison of cell lysates. The proteins can be used as biochemical markers to detect the phase of the endometrium and can be measured in body fluids, obviating the need for endometrial biopsies.
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W54351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
W09810291-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
2D gel electrophoresis; detection.
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                                                                                                                                                                                                                                                                                231 aflkklheeeigel 244
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                                                                                                                                                                                                                                             5 SFIRTAHDSEVQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 465
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Similarity 35.78;
5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         465 AA;
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                                                                                                                                                                                                                                                                                                               Score 60; DB 31; LA
Pred. No. 3.53e+01;
6; Mismatches 3;
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Pred. No. 3.53e+01
8; Mismatches
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production;

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PN J09173074-A.

PD 08-JUL-1997.

PF 21-DEC-1995; 349914.

PR 21-DEC-1995; JP-349914.

PA (MAZN) COSMO SOGO KENKYUSHO KK.

PA (COSM-) COSMO SOGO KENKYUSHO

PT POTOL COSMO SOGO

PT
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Search completed: Tue Jan 11 15:41:38 2000 Job time : 21 secs.

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就跟我们的我的我们的现在分词 医克勒特氏 医克勒特氏病 医多种性皮肤 医多种皮肤 医多种皮肤皮肤 医多种皮肤皮肤 医多种皮肤皮肤 医多种皮肤皮肤 医多种皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤皮肤	[] [] [] [] [] [] [] [] [] []	

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:46:03 2000; MasPar time 1.64 Seconds 145.493 Million cell updates/sec

lar output not generated.

Description: Perfect Score: Sequence: >US-09-290-049-2 (1-20) from US09290049.pep 135 1 VPSYSFIRTAHDSEVQDLIA 20

Scoring table: PAM 150 Gap 15

Searched: 122461 seqs, 11912985 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 19.113; Variance 59.268; scale 0.322

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. N	No.
1	61	45.2	344	2	US-08-689-	Sequence 1, Applicatio	1.38e	<u></u>
2	57		160	N	-08-72	183	ω	ġ
ω	57	42.2	494	N		3, Ap	· ω	Ċ
4	56	•	366	N	us-08-690-	96, App	4	Ė
ر. ن	55		256	N	US-08-469-	58,	۲ 5.	Ė
6	55	40.7	266	N	US-07-857-	75,	5	Ċ
7	55	40.7	282	N	US-08-701-	Sequence 19, Applicati		Ċ
80	55	40.7	1003	N	US-07-743-	~	s	Ė
9	54	•	244	N	US-08-553-	'n	7	Ċ
10	54	•	244	N	US-08-737-	'n	7	Ċ
11	54	•	473	N	US-08-746-	13,	7	ģ
12	54	•	473	_	US-08-597-	13,	7	ģ
13	54	40.0	1069	N	US-08-162-	37,	cati 7.33e+01	ġ
14	54	•	1069	N	US-08-780-	37,	cat1 7.33e+01	음
15	54	•	1080	N	US-08-780-	36,	. 7	ė
16	54	•	1080	N	US-08-162-	36,	cati 7.33e+01	ģ
17	53	•	980	_	US-08-413-	5,	9	ģ
18	53	•	980	Н	US-08-220-	Sequence 5, Applicatio	9	ဂ္ဂ
19	53	•	1172	N	US-08-313-	Sequence 19, Applicati	cati 9.24e+01	ġ
20	52		418	ω	PCT-US94-0	72,	cat1 1.16e+02	2
21	52		865	<u>, </u>	US-07-803-	Sequence 13, Applicati	cati 1.16e+02	ဂ် လ
22	52	38.5	913	N	US-07-743-	22,	cat1 1.16e+02	ဂ် သ
23	52	38.5	913	N	US-07-743-	Sequence 6, Applicatio	atio 1.16e+02	02

45	44	43	42	41	0	39	38	37	36	35	34	ω	32	31	30	29	28	27	26	25	24	
51	51	51	51	51	51	51	51	51	51	51	51	51	٠ 51	51	52	52	52	52	52	52	52	
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1139	1139	1082	788	718	598	456	455	445	445	393	375	375	221	221	1016	1016	1016	1005	1004	1003	1003	
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US-08-832-	US-08-832-	US-08-106-	US-07-728-	US-08-445-	US-08-937-	PCT-US95-1	US-08-349-	US-08-838-	US-08-630-	us-08-689-	US-08-027-	US-08-027-	us-08-773-	US-08-916-	US-07-743-	US-07-743-	US-07-743-	US-07-743-	US-07-743-	US-07-743-	US-07-743-	
	Sequence 2	Sequence 2	Sequence 3		Sequence 2	Sequence 4,	Sequence 4,	Sequence 6,	Sequence 6	Sequence 4		Sequence 2,	Sequence 7	Sequence 9	Sequence 4	Sequence 3	Sequence 2	Sequence 1	Sequence 7	Sequence 8	Sequence 10	
•	`	` `	 32, Applicati 	•					`	, Applicatio	•		•	`	, Applicatio	•	•	, Applicatio	, Applicatio	, Applicatio	 Applicati 	
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ALIGNMENTS

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IMMEDIATE SOURCE:	. !	2	EDNESS	amino acid	LENGTH: 344 amino acids	SEQUENCE CHARACTERISTICS:		TELEFAX: 415-845-4166	日は1日は1916年 はは、ついり、はいい		TON	딾	REGISTRATION NUMBER: 36,749	NAME: Billings, Lucy J.	ATTORNEY/AGENT INFORMATION:	FILING DATE: Filed Herewith	APPLICATION NUMBER: US/08/689,974	CURRENT APPLICATION DATA:	SOFTWARE: FastSEQ Version 1.5	SYSTEM: DOS	COMPUTER: IBM Compatible	띪	COMPUTER READABLE FORM:	94304	COUNTRY: U.S.	Ω	CITY: Palo Alto	STREET: 3174 Porter Drive	ADDRESSEE: Incyte Pharmaceuticals, Inc.	CORRESPONDENCE ADDRESS:	NUMBER OF SEQUENCES: 5	TITLE OF INVENTION: NOVEL HUMAN INDUCED TUMOR PROTEIN	Murray, Lynn E.	Hawkins, F	APPLICANT: Au-Young, Janice		5776732	Sequence 1, Application US/08689974		Sequence 1, Application US/08689974				XXXXXX		80-2	

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Best Local Similarity 53.38;
                                                    Query Match
Best Local Similarity
Matches 5; Conser
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CLONE: 530522
SEQUENCE 344 AA; 3
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                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 183, Application US/08726306A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 183, April No. 5958684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221 YSSIRTSNNSQVNKL 235
                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9110
TELEPAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 183:
                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05-Oct-1996
PRIOR APPLICATION NUMBER: 05-Oct-1996
PRIOR APPLICATION NUMBER: 05-Oct-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 YSFIRTAHDSEVQDL 18
                                                                                               TOPOLOGY: unknown MOLECULE TYPE: peptide Series 160 AA; 17935 MW; 109819 CN;
                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 9
FILING DATE: 02-Oct-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
                    SFLKKVHEEEIAEL
                                                                                                                                              TYPE: amino acid
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STREET: 1 Financial Center
                                                                                                                                   STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banner & Witcoff, Ltd
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                                                                42.28;
35.78;
                                                                                                                                   single
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Pred. No. 1.38e+01;
                                                               Score 57; DB 2; I
Pred. No. 3.61e+01;
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                                                                          Length 160;
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Best Local Similarity 53.3%;
Matches 8; Conservative
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                    Sequence 96, Application US/08690734A
                                                                               US-08-690-734A-96
                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08689974
                                                                                                                               350 YSSIRTSTNSQVDKL 364
 Sequence 96, Application US/08690734A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                                                                                                                                                                                TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                      4
                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: pept:
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1293563
                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEEO VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Au-Young, Janice
APPLICANT: Hawkins, Phillip R.
APPLICANT: MUITAY, Lynn E.
TITLE OF INVENTION: NOVEL HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                     YSFIRTAHDSEVQDL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFIRTAHDSEVQDL
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                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/6 FILING DATE: Filed Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U
ZIP: 94304
                                                                                                                                                                                                                                                                   TYPE: amino acid
                                                                                                                                                                                                                                                                                                                   TELEPHONE:
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                                                                                                                                                                                                 494 AA; 54746 MW; 1410529 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.
                                                                                                                                                                                                                                                                              494 amino acids
                                                                                                                                                                                                                                                                                                                      415-855-0555
                                                                                                                                                                                                                                        peptide
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                                                                               STANDARD;
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                                                                                                                                                                   Score 57; I
Pred. No. 3
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3.61e+01;
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                                                                               366 AA
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Best Local Similarity
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                                                                                                                                                                       Sequence 58, Application US/08469537A
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                                                                                                                                        Sequence 58, Application US/08469537A Patent No. 5843749
                                                                              GENERAL INFORMATION:
APPLICANT: MAISODPIETE, et
TITLE OF INVENTION: EHK AND
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
                                                                                                                                                                                                                                                                                                            81 GYGFVSFVNDVDVQKIVG 98
                                                                                                                                                                                                                                                                                       3 SYSFIRTAHDSEVQDLIA 20
                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/3:
FILING DATE: 22-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Page, David C. APPLICANT: Reijo, Renee TITLE OF INVENTION: DAZ: A NUMBER OF SEQUENCES: 96 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
JENCE 366 AA; 41236 MW; 802697 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: WHI94-07A TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 861-6240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/690,734A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                              STREET: 777 O10
CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
   COUNTRY: U.S.A. ZIP: 10591
                          STATE:
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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WENTION: EHK AND ROR TYROSINE
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Pred. No. 4.58e+01
8; Mismatches !
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                                                                                                                                                                                                                                                              Sequence 75, Application US/07857224B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                             Sequence 75, Application US/07857224B Patent No. 5958784
                                                                                                                                                                                                             Patent No. 5958784
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                              5 SFIRT-AHDSEVODLIA 20
     SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette,
COMPUTER: Apple MacIntosh
OPERATING SYSTEM: MacIntosh 7.0
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
                                                                                                                                                                              APPLICANT: Benner, STITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
JENCE 256 AA; 29258 MW; 364977 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 256 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail |
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REV
                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
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                                                                                                                         STREET: Hadla
CITY: Zurich
STATE: none
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                            COUNTRY: Switzerland ZIP: (note: this is an international post code) CH-8092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: sing TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
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                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 914-345-7721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                         h 40.7%;
Similarity 47.1%;
8; Conservative
                                                                                                                                             E: Steven A. Benner
Hadlaubstrasse 151
                                                                                                                                                                                                     Benner, Steven A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                 STANDARD;
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Pred. No. 5.80e+01;
5; Mismatches 3
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                                                                            1.4 Mb storage
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PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:

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Best Local Similarity 47.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                             Sequence 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                      92 NFIRNETHNPTVKDLIG 108 : | | | : | : | | | | | :
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                                                                                                                                                                                                                                                                                tent No.
                                                                                            COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                           NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon 6 Lyon
                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS
SOFTWARE: FastSEO for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: human FEATURE: Protein kinase; Table 8 Column PUBLICATION INFORMATION:
                                                                                                                                                                                                                                           APPLICANT: Moosa Monammagi, Justi
APPLICANT: and Stevan R. Hubbard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                            TITLE OF INVENTION: CRYSTALS OF THE TYROSINE KINASE DOMAIN
                    APPLICATION NUMBER: FILING DATE: August CLASSIFICATION: 530
                                                                                                                                                 STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAGES: 42-52
DATE: 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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                                                                                                                                                                                                                                                                       INFORMATION:
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                                                                                                                                                                                                                                                                                             Application US/08701191A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (International) 41 1 632 2830 (International) 41 1 262 2437
                                                                                                                                                                                                                                                           Moosa Mohammadi, Joseph Schlessinger,
                           UMBER: US/08/701,191A
August 21, 1996
                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 2; I
Pred. No. 5.80e+01;
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Best Local S
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application US/07743357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          XXXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 9, Application US/07743357
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                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                       APPLICATION NUMBER: US/07/743,357
FILING DATE: 21-AUG-1991
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA90/00062
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gale, Edwin J
REGISTRATION NUMBER: 28,584
                     INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 40.7%;
Local Similarity 47.1%;
les 8; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 SFIRT-AHDSEVQDLIA 20
                                            REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (613) 237-6900
TELEPHAX: (613) 237-0045
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE BAKER
STREET: Box 3432, Station D
                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
TITLE OF INVENTION: activity for use as diagnostic r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                    COUNTRY: Canada
ZIP: Klm 1H8
                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                      CITY: Ottawa
            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION:
amino acid
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67-3510
                                                                                                                                                                                                                                                                                          Ontario
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            1003 amino acids
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Pred. No. 5.80e+01;
5; Mismatches 3
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                      SEQUENCE
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SEQUENCE 10
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Local Similarity 40.0%;
                                                                                                       INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)-205-8000
TELEFAX: (703)-205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                        MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SYENSSON, LEONARD R
REGISTRATION NUMBER: 30,33
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/553,633A
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, ST
                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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TOPOLOGY: not
                                                              TOPOLOGY:
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                                ORGANISM:
                                                                                  LENGTH:
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                  IISM: Erwinia carotovora
244 AA; 28137 MW; 305391 CN;
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                                                                      d: 244 amino acids amino acid
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MCGOMAN, SIMON J
AVENTION: PROCESS FOR ACTIVATING GENE EXPRESSION
AVENTION: IN BACTERIA
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                                                                                                                                                                                                                                                                                                USA
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                                                             linear
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                                                  protein
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40.0%;
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Pred. No.
Score 54;
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Length 244;
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Matches 6; Conser
                     Matches
                              Query Match 40.0%;
Best Local Similarity 35.3%;
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                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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98 SGYTFVLHDHDNNVATL 114
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                                                                                                                                                                              TELEX: 248345
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: MICROSOFT WORD97
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 205-8000
                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                             ANTI-SENSE:
                                                                                                      HYPOTHET ICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 03-JUN
                                                            ORGANISM: Erwinia carotovora
ICE 244 AA; 28137 MW; 305391 CN;
                                                                                                                                                                                                                                                                                                                                                                                                     STREET: P.O. Box 7
CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLE OF
                                                                                                                                  STRANDEDNESS:
                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                   TELEFAX:
                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                           OPOLOGY:
                                                                                                                                                         ENGTH:
                     6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08737825
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Conservative
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVENTION: GENES INVOLVED IN THE BIOSYNTHETIC PATHWAY OF CARBAPENE
                                                                                                                                                       244 amino acids
                                                                                                                                                                                                 (703) 205-8050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COX, ANTHONY RICHARD JOHN HOLDEN, MATTHEW THOMAS GEN PORTER, LAUREN ELIZABETH BYCROFT, BARRIE WALSHAM
                                                                                             ğ
                                                                                                                                                                                                                                                                                                                           IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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: 03-UN-1997
TON: 435
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                  Score 54; DB 2; I
Pred. No. 7.33e+01;
6; Mismatches 5
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                                       Length 244;
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Best Local Similarity
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US-08-746-682A-13
                                                              XXXXXX
                                                                               US-08-597-236-13
                         Sequence 13, Application US/08597236
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Sequence 13, Application US/08597236 Patent No. 5733765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GRAPHICANT: STINGELE, Franscesca
APPLICANT: MOLLET, Beat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent No.
                                                                                                                                 29 VPLYTYAMTPQEYGMADL 46
                                                                                                                                                                                                                                           REGISTRATION NUMBER: INFORMATION FOR SEQ ID NO:
                                                                                                                  1 VPSYSFIRTAHDSEVQDL 18
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/597,236
FILING DATE: 20-JUN-1995
APPLICATION NUMBER: EP 9520166:
                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acids
                                                                                                                                                                                                                                                   FILING DATE: 20-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fanucci A., Allan
REGISTRATION NUMBER: 30256
                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSYSFIRTAHDSEVQDL 18
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/746,682A FILING DATE: 14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
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                                                                                                                                                                                                         TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                  New York
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1155 Avenue of the Americans
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                                                                               STANDARD;
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Pred. No. 7.33e+01
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Best Local Similarity
Matches 6; Conser
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CLASSIFICATION: 426

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 9520166'

PILING DATE: 20-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: FABRUCCI A., Allan

TOTSTERATION NUMBER: 30256

TOTSTERATION NUMBER: 30256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VPSYSFIRTAHDSEVQDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 473 amino acid
TYPE: amino acid
TYPE: amino acid
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APPLICANT: MOLLET, Beat
TITLE OF INVENTION: LAC
TITLE OF INVENTION: EXC
COMPUTER READABLE FORM: mEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                        APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhano APPLICANT: Bala; Waterfield, Michael Derek; Parker, PappLICANT: Joseph; Otsu, Masayuki; Panayotou, George;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                COUNTRY: U
ZIP: 10022
                                                                         CITY: New York
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                                                          New York
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805 Third Avenue
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Pred. No. 7.33e+01
6; Mismatches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    Sequence 37, Application US/08780872 Patent No. 5846824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 22.2%; hes 4; Conservative
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TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 37
                                                                                                                                                                                                                                                                                                                                                      GENERAL
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TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY, TITLE OF INVENTION: THEIR PREPARATION AND USE NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1069 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DO
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                             OPERATING SYSTEM: PC-DOS
SOFTWARE: WOrdperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,872
FILING DATE: 09-JAN-1997
                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13 APT11 1993
ATTOKNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: LUD 5256 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                             CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: linear
NCE 1069 AA; 124437 MW; 5707845 CN;
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FILING DATE: February APPLICATION NUMBER:
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                                                                                                                                                                                  COUNTRY:
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February 7, 1994
UMBER: PCT/GB93/00761
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Pred. No. 7.33e+01;
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                                                      FILING DATE: 09-TAN-1997

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 APRIL 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patticia A.
REGISTRATION NUMBER: 34,894
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette, 5
COMPUTER: IBM PS/2
COPERATING SYSTEM: PC-DOS
SOFTWARE: WORDDERFIECT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OFTERED
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                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                   TELEPHONE: (212) 688-9200
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APPLICANT: Stefano; Gout, Ivan Tarasovitch
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                            REFERENCE/DOCKET NUMBER:
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805 Third Avenue
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Bala; Waterfield, Michael Derek; Parker, Peter
Joseph; Otsu, Masayuki; Panayotou, George; Volini;
            (212) 838-3884
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Pred. No. 7.33e+01;
10; Mismatches 4
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Search completed: Tue Jan 11 15:46:11 2000 time: 8 secs.	Db 66 SSYIFVSVTQEAEREEFF 83	Query Match 40.0%; Score 54; DB 2; Length 1080; Best Local Similarity 22.2%; Pred. No. 7.33e+01; Matches 4; Conservative 10; Mismatches 4; Indels 0; Gaps 0;	CC SEQUENCE CHARACTERISTICS: CC LENGTH: 1080 amino acids CC TYPE: amino acid CC STRANDEDNESS: single CC TOPOLOGY: linear SQ SEQUENCE 1080 AA; 125733 MW; 5831251 CN;

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: ar output not generated. Tue Jan 11 15:41:54 2000; MasPar time 3.73 Seconds 214.842 Million cell updates/sec

Scoring table: Description: Perfect Score: Title: >US-09-290-049-2 (1-20) from US09290049.pep 135 1 VPSYSFIRTAHDSEVQDLIA 20

Searched: PAM 150 Gap 15

122810 segs, 40068593 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database:

pir60 1:pir1 2:pir2 3:pir3 4:pir4

Statistics: Mean 28.511; Variance 41.538; scale 0.686

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Query Query Query Query Query Query Query Antch Length DB ID Description Pred. No. 115 85.2 1475 2 B33135 116 82.2 1375 2 JT0345 97 71.9 1592 2 A38175 86 63.7 1365 2 A41483 78 57.8 1312 2 A45866 63.7 1365 2 A444831 79 58.5 1431 2 A45866 1518 2 A44831 174 54.8 1599 2 \$22737 175 57.0 1518 2 A44811 176 53.3 101 2 \$252737 177 52.6 532 1 QFPGM 170 52.6 916 2 A27864 170 51.9 494 2 152658 170 51.9 504 2 A47866 170 51.9 504 2 152658 170 51.9 504 2 152658 170 51.9 504 2 152658 170 51.9 504 2 153868 170 51.9 504 2 153868 170 51.9 504 2 153868 170 51.9 504 2 153868 170 51.9 505 2 A41023 170 51.9 504 2 153868 170 51.9 505 2 A41023 170 51.9 506 2 150479 171 52.6 6 1849 2 \$00030 171 52.6 916 2 A27864 172 173868 173 174 175 175 175 175 175 175 175 175 175 175
Length DB ID Description 1475 2 B33135 1375 2 JT0345 dextransucrase (EC 2. 3 1592 2 A38175 1365 2 A41483 glucosyltransferase p 1290 2 JC5473 dextransucrase (EC 2. 3 1365 2 A44813 1518 2 A44811 1518 2 A44811 1518 2 A44811 1519 2 S22737 101 2 S51349 hypothetical protein p 101 2 S51349 hypothetical protein p 102 A45864 103 1 A45864 104 2 I52658 105 2 A7864 105 2 A7864 107 2 A78664 108 2 A78664 109 2 B7864 109 2 B7868 109 2 B7868 100 2 B7868 1
DB ID Description Pr B33135 gtfB protein precurso 4 JT0345 dextransucrase (EC 2. 3 A488175 glucosyltransferase p 2 JC5473 dextransucrase (EC 2. 3 A441483 glucosyltransferase (EC 2. 2 A448811 glucosyltransferase (EC 2. 2 S46329 intermediate filament 5 2 A45866 dextransucrase (EC 2. 2 S46329 incosyltransferase (5 S25737 glucosyltransferase (5 S25739 protein 2 S251349 hypothetical protein 2 S251349 hypothetical protein 6 A45669 neurofilament triplet 8 A77864 neurofilament triplet 8 A1023 alpha-internexin - mo 1 A41023 alpha-internexin - mo 1 A41023 alpha-internexin - mo 1 S28296 neurofilament triplet 4 S150479 neurofilament triplet 4 S15762 intermediate filament 1
B33135 gtfB protein precurso 4 JT0345 dextransucrase (EC 2. 3 A38175 glucosyltransferase p JC5473 dextransucrase (EC 2. 3 A41483 glucosyltransferase (EC 2. 3 A41481 glucosyltransferase (EC 2. 3 A46329 intermediate filament A44811 glucosyltransferase (S53395 glucosyltransferase (S53395 neurofilament protein 22737 glucosyltransferase (S53349 hypothetical protein S27349 neurofilament triplet 8 A27864 neurofilament triplet 8 A27864 neurofilament triplet 8 A27864 neurofilament triplet 8 A27864 neurofilament triplet 8 A27868 alpha-internexin - m 1 S38296 alpha-internexin - m 1 S38296 neurofilament triplet 8 A1023 alpha-internexin - m 1 S28296 neurofilament triplet 8 S28296 neurofilament triplet 8 S28296 neurofilament triplet 4 S35762 intermediate filament 4 S41720 intermediate filament
gtfB protein precurso dextransucrase (EC 2. 3 glucosyltransferase pducosyltransferase (EC 2. 1 glucosyltransferase pducosyltransferase pducosyltra
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Pred. No. 4.19e-111 3.42e-10 5.15e-05 9.30e-05 9.30e-05 9.32e-02 2.32e-02 2.32e-02 2.32e-02 8.62e-02 8.62e-02 8.62e-02 1.33e-01

JT0345 #type complete
dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans
(strain GS-5)

45	44	43	42	41	40	39	38	37	36	35	ω 4	33	32	31	30	29	28	27	26	25	
61	61	61	61	61	61	61	61	61	61	62	62	62	62	62	62	63	63	63	63	64	
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matrix metalloprotein	matrix metalloprotein	matrix metalloprotein	vimentin - mouse	vimentin - rat	YMK1 protein - yeast	vimentin - Chinese ha	glial fibrillary acid	glial fibrillary acid	probable P26 – syphil			RNA-binding protein T	hypothetical protein	T-cluster binding pro	cytochrome P450 (CYP4	B	glycoprotein B precur	tein B		cysteine proteinase A	
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ALIGNMENTS

Db 552 VPSYSFI Qy 1 VPSYSFI RESULT 2 ENTRY TITLE	Query Match Best Local Similarity Matches 19; Conse	124-115 124-1243 128-1308 1354-1373 1419-1438 SUMMARY	##status ##molecule_type ##residues ##experimental_: CLASSIFICATION #sup	##residues ##cross-rei REFERENCE REFERENCE #authors #submission #accession	REFERENCE A331 #authors Shire #journal J. Ba #title Seque #cross-references #accession B331: #accessian b331:	RESULT 1 ENTRY TITLE ORGANISM DATE ACCESSIONS
VPSYSFIR-AHDSEVQDLIA 570	85.2%; Score 115; DB 2; Length 1475; ilarity 95.0%; Pred. No. 4.19e-11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;	#domain cpl repeat homology #label CPl\ #domain cpl repeat homology #label CP2\ #domain cpl repeat homology #label CP3\ #domain cpl repeat homology #label CP4\ #domain cpl repeat homology #label CP4\ #domain cpl repeat homology #label CP5 #length 1475 #molecular-weight 165811 #checksum 7497	##status preliminary; not compared with conceptual translation ##molecule_type DNA ##residues 1-171,173-641,'N',643-1475 ##label SH2 ##experimental_source strain GS-5 ##experimental_source strain GS-5 #FICATION #superfamily cpl repeat homology	##residues 1-1475 ##label SHI ##cross-references GB:M17361; NID:g153639; PID:g153640 RCE A33128 thors Shiroza, T.; Ueda, S.; Kuramitsu, H.K. bmlssion submitted to the Protein Sequence Database, September 1990 cession A33128	#A33135 #authors Shiroza, T.; Ueda, S.; Kuramitsu, H.K. #authors Shiroza, T.; Ueda, S.; Kuramitsu, H.K. #journal J. Bacteriol. (1987) 169:4263-4270 #title Sequence analysis of the gtfB gene from Streptococcus mutans. #cross-references MUID:87308013 #accession B3315 ##status preliminary ##molecule_type DNA	B33135 #type complete gtfB protein precursor - Streptococcus mutans #formal_name Streptococcus mutans 23-Oct.1990 #sequence_revision 23-Oct.1990 #text_change 09-Sep-1997 B33135; A33128

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ACCESSIONS
REFERENCE
#authors
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ENTRY
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FEATURE
                      CLASSIFICATION
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REFERENCE
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1253-1272
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35-1375
                                                                                                                          #title Peptide sequences for sucrose splitting and glucan binding within Streptococcus sobrinus glucosyltransferase (water-insoluble glucan synthetase).
#cross-references_MUID:91123227
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Journal J. Bacteriol. (1987) 169:4263-4276
Fittle Sequence analysis of the gtfB gene
bross-references MUID:87308013
                                                                                                                                                                                                                                                                                                                                                                                                                                                               578 VPSYSFIR-AHDSEVQDLI 595
                                   ##cross-references GB:D90213; NID:g217032; PID:d1014946; PID:g217033
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Gene (1996) 182:23-32
Cloning and sequencing of a gene coding for a novel Cloning and sequencing of a gene coding for a novel dextransucrase from Leuconostoc mesenteroides NRRL B-121 dextra
                                                          Gilmore, K.S.; Russell, R.R.B.; Ferretti, Infect. Immun. (1990) 58:2452-2458
Analysis of the Streptococcus downel gtfs specifies a glucosyltransferase that syn
                                                                                                                                                                                                                                                                                                                   Streptococcus sobrinus
#formal_name Streptococcus sobrinus
30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change
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dextransucrase (EC 2.4.1.5) - Leuconostoc mesenteroides
#formal_name Leuconostoc mesenteroides
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Pred. No. 4.36e-07;
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15; Conservative
                         Dodemont, H.; Riemer, D.; Ledger, N.; Weber, K.
EMBO J. (1994) 13:2625-2638
Eight genes and alternative RNA processing pathways generate
an unexpectedly large diversity of cytoplasmic intermediate
filament proteins in the nematode Caenorhabditis elegans.
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J. Gen. Microbiol. (1990) 136:2099-2105
Nucleotide sequence of the Streptococcus mutans gtfD
encoding the glucosyltransferase-S enzyme.
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#formal_name Streptococcus mutans
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intermediate filament protein - Caenorhabditis elegans
#formal_name Caenorhabditis elegans
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##cross-references EMBL:Z11873; NID:g47526; PID:g47527
##note sequence extracted from NCBI backbone
NCBIP:81052)
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                                                                           Vitadello, M.; Vettore, S.; Lamar, E.; Chien submitted to the EMBL Data Library, January Neurofilament mRNA and protein are expressed heart conduction myocytes.
                                                                                                                                        S55395
S55395
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Molecular characterization of a cluster of at least two
                                                                                                                                                                   15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 08_Sep-1997
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glucosyltransferase (EC 2.4.1.-) I - Streptococcus salivarius
#formal_name Streptococcus salivarius
31-pec-1993 #sequence_revision 31-Dec-1993 #text_change
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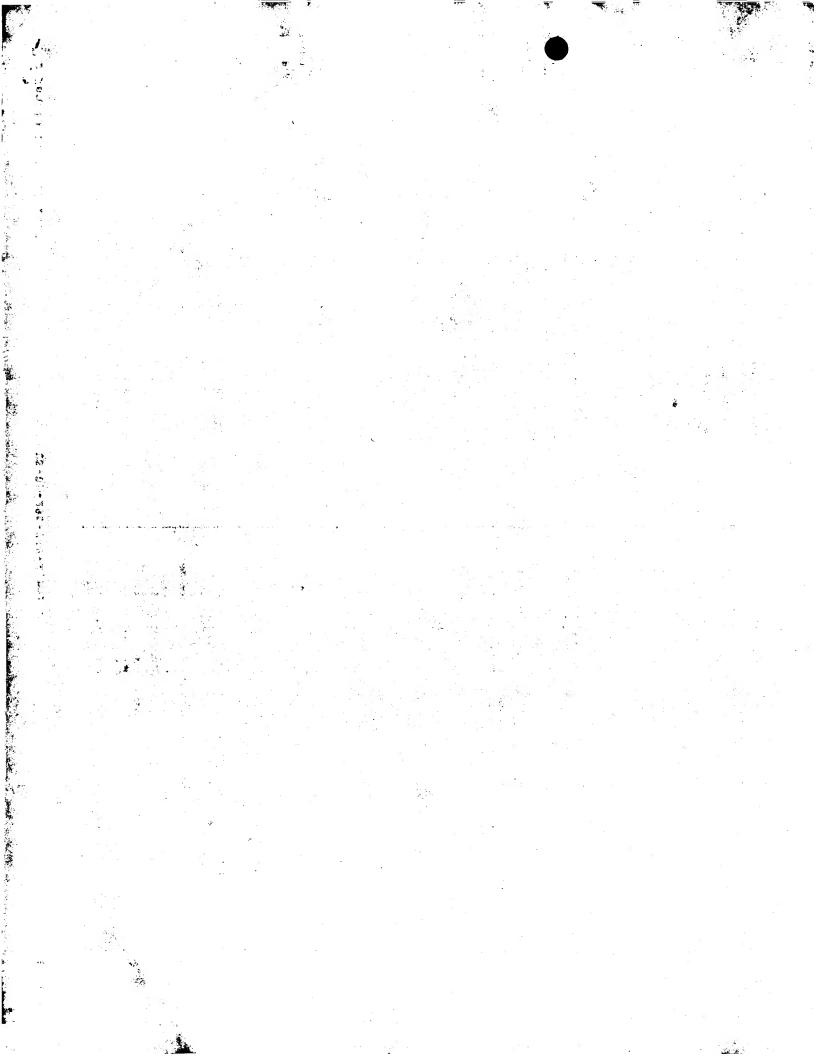
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#authors
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#accession S28810
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##cross-references EMBL:211872; NID:g47530;
                                                                      #molecule_type DNA
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Similarity 63.2%;
12; Conservative
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S51338
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                                                                                        submitted to the The sequence of S $51349
                                                                                                                                                                              hypothetical protein L8300.14
#formal_name Saccharomyces cerevisiae
23-Feb-1995 #sequence_revision 12-May-1995 #text_change
21-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                #superfamily cpl repeat homology
glycosyltransferase; hexosyltransferase
#length 1599 #molecular-weight 176480
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Molecular characterization of a cluster of at least two
                                                                                                                                     Du,
                                                                                                                                                                                                                                                    S51349 #type complete hypothetical protein YLR346c -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacques, N. submitted to the S22737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      $22737  #type complete glucosyltransferase (EC 2.4.1.-) S - Streptococcus salivarius #formal_name Streptococcus salivarius 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change
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2737; S28810; B44811; S22727
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#checksum 9233
#molecular-weight 11348
                                                                                                     e EMBL Data Library, December S. cerevisiae cosmid 8300.
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Pred. No. 2.32e-02
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Pred. No. 2.32e-02;
4; Mismatches 3
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#title Hybrid character of a large neurofilament protein (NF-M):
    intermediate filament type sequence followed by a long a cidic carboxy-terminal extension.
#cross-references_MUID:85076594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #authors Geisler, N.; Vandekerckhove, J.; Weber, K.
#journal FEBS Lett. (1987) 221:403-407
#title Location and sequence characterization of the
phosphorylation sites of the high molecular
neurofilament proteins M and H.
#cross-references MIDD:87304852
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460-475,476-514
515-532
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NCE S02570
thors
                                                                                                                                                                      232 AFLRSNHEEEVADLLA 247 :|:|: |: || ||:|
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##residues 438-450;455-459;460-475;476-514;515-532 ##label GEI2
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Local Similarity 50.0%;
Les 8; Conservative
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                         A45669 #type complete
neurofilament triplet M protein - rat
#formal_name Rattus norvegicus #common
31-Dec-1993 #sequence_revision 31-Dec-
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neurofilament triplet M protein - pig (fragments)
160K neurofilament protein; NF-M(medium) protein;
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31_Mar-1988 #sequence_revision 02-Jul-1998 #text_change
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gth 532  #checksum 5520
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#modified_site blocked amino end (Ser) (probably
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Pred. No. 5.
12; Mismatc
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Pred. No. 8.62e-02;
5; Mismatches 3
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31-Dec-1993 #text_change
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#accession A27864
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#accession A42393
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##cross-references GB:Y00067;
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##residues 411-500, Fr. 501-843, 'D' ##label XU1
##residues sequence extracted from NCBI backbone (NCBIP:83873)
##nOte sequence extracted keratin
#ICATION #Superfamily cytoskeletal keratin
#Inspecial #I
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##molecule_type mRNA
##residues 1-17,19-21,'P',23-204,'L',206-500,'E',501-845 ##label
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Local Similarity 50.0%;
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J. Biol. Chem. (1992) 267:4467-4471
Identification of six phosphorylation sites in the
COOH-terminal tail region of the rat neurofilament protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A45669
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Complete amino acid sequence and in vitro expression of rat NF-M. the middle molecular weight neurofilament protein.
Lee, V.M.Y.; Otvos Jr., L.; Carden, M.J.; Hollosi, M.; Dietzschold, B.; Lazzarini, R.A.
Proc. Natl. Acad. Sci. U.S.A. (1988) 85:1998-2002
Identification of the major multiphosphorylation site
                                                                                                                                                                                                                                                                                                                                                                       The human mid-size neurofilament subunit: a sequence and the relationship of its gene intermediate filament gene family.
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EMBO J. (1987) 6:1617-1626
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30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change
20-Mar-1998
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Pred. No. 8.62e-02;
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NID:g35045; PID:g35046
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#accession I52658
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                                                                                                                                                                        ##cross-references GB:S78296; NID:g994843; PID:g994844
FICATION #superfamily cytoskeletal keratin
Y #length 494 #molecular----/
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                                                                                        221 AFVRQVHDEEVAELLA 236
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Similarity 50.0%;
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Brain Res. Mol. Brain Res. (1995) 29:177-184
Cloning and developmental expression of human
neurofilament protein.
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coiled coil; phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                         #formal_name Homo sapiens #common_name man 02-Jul-1996 #sequence_revision 02-Jul-1996
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neurofilament-66 - human
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    predicted
jth 916    #molecular-weight 102447    #checksum 8997
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4; Misma
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Pred. No. 8.62e-02
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No. 1.33e-01;
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:42:29 2000; MasPar time 2.40 Seconds 235.764 Million cell updates/sec

ar output not generated.

Title: >US-09-290-049-2
Description: (1-20) from US09290049.pep
Perfect Score: 135

Sequence: 1 VPSYSFIRTAHDSEVQDLIA 20

Scoring table: PAM 150 Gap 15

Searched: 77977 seqs, 28268293 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: swiss-prot37
1:swissprot

Statistics: Mean 29.305; Variance 37.765; scale 0.776

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	B	ID	Description	Pred. No.
	115	85.2	1475	ᆸ	GTFB_STRMU	GLUCOSYLTRANSFERASE-I	9.14e-13
2	111	82.2	1375	ᆫ	GTFC_STRMU	GLUCOSYLTRANSFERASE-SI	9.54e-12
ω	103	76.3	1597	\vdash	GTF1_STRDO	GLUCOSYLTRANSFERASE-I	9.56e-10
4	97	71.9	1592	μ.	GTF2_STRDO	GLUCOSYLTRANSFERASE-I	2.79e-08
s	86		1365	۲,	GTFS_STRDO	GLUCOSYLTRANSFERASE-S	
6	79	•	1430	μ.	GTFD_STRMU	GLUCOSYLTRANSFERASE-S	4.10e-04
7	74	54.8	644	<u>س</u>	NFM_RABIT	NEUROFILAMENT TRIPLET	4.97e-03
œ	71		454	۲	NFM_PIG		2.12e-02
9	71		845	ш	NFM_RAT		2.12e-02
10	71	52.6	915	۲	NFM_HUMAN	NEUROFILAMENT TRIPLET	H
11	70	•	504	۳	AINX_MOUSE	ALPHA-INTERNEXIN (ALPH	w
12	70	51.9	505	<u>س</u>	AINX_RAT		ω.
13	68	•	372	ب	YLF1_CAEEL	HYPOTHETICAL 42.4 KD P	œ
14	67	49.6	848	μ	NFM_MOUSE	NEUROFILAMENT TRIPLET	1.39e-01
15	67	49.6	857	ب	NFM_CHICK	NEUROFILAMENT TRIPLET	1.39e-01
16	64	47.4	465	μ	VIME_BOVIN	VIMENTIN.	5.43e-01
17	63	46.7	873	۳	VGLB_ILTV6	GLYCOPROTEIN B PRECURS	8.48e-01
18	63	46.7	883	4	VGLB_ILTVS	GLYCOPROTEIN B PRECURS	8.48e-01
19	63	46.7	883	μ.	VGLB_ILTVT		
20	62	45.9	375	<u>ب</u>	TIAR_HUMAN	NUCLEOLYSIN TIAR (TIA-	1.32e+00
21	62	45.9	386	_	TIA1_MOUSE	TIA-1	1.32e+00
22	62	45.9	392	_	TIAR_MOUSE	TIAR (1.32e+00
23	61	45.2	428	_	GFAP_BOVIN	GLIAL FIBRILLARY ACIDI	2.03e+00

EMBL; M17361; G153640; PIR; B33135; B33135.
PFAM; PF00128; alpha-amylase; 1.
TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.
SIGNAL 1 34 POTENTIAL.

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	4.7
58	58	58	58	58	59	59	59	59	60	60	60	61	61	61	61	61	61	61	61	61	ō
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CARBON MONOXIDE DEHYDR	INTERMEDIATE FILAMENT	HYPOTHETICAL 30.0 KD P	CHLOROPLAST 28 KD RIBO	30S RIBOSOMAL PROTEIN	GENERAL NEGATIVE REGUL	PROBABLE 6-PHOSPHOFRUC	NEOPULLULANASE (EC 3.2	KERATIN, TYPE I CYTOSK	LOW MOLECULAR WEIGHT N	VIMENTIN.	NUCLEOLYSIN TIA-1.	MATRIX METALLOPROTEINA	MATRIX METALLOPROTEINA	MATRIX METALLOPROTEINA	VIMENTIN.	VIMENTIN.	VIMENTIN.	HYPOTHETICAL 49.2 KD P	VIMENTIN (FRAGMENT).	GLIAL FIBRILLARY ACIDI	GLIAL FIBRILLARY ACTUL
7.24e+00	7.24e+00	7.24e+00	7.24e+00	7.24e+00	4.77e+00	4.77e+00	4.77e+00	4.77e+00	3.12e+00	3.12e+00	3.12e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00	2.03e+00

ALIGNMENTS

RESULT ID G	LT 1 GTFB_STRMU STANDARD; PRT; 1475 AA.
AC	
33	1988 (REL. 09, CREA
DI.	15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
멾	GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5) (GTF-I) (DEXTRANSUCRASE)
a B	NOSE 6-GLUCOSYLTRANSFERASE).
8 8	STREPTOCOCCUS MUTANS.
გ	BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP; STREPTOCOCCACEAE;
8	STREPTOCOCCUS.
R	[1]
3 2	SEQUENCE FROM N.A.
₹ :	MEDLINE; 87308013.
₽₽	SHIROZA T., UEDA S., KURAMITSU H.K.;
R ?	J. BACTERIOL. 169:4263-4270/1987).
38	-!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
36	OF THE STATE OF THE TAX ADDITION OF THE CONTROL OF
នន	AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
8	-!- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) -
38	
88	-1- DISEASE: DENTAL CARIES.
ဂ	-!- GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED
88	GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
ဂ	
ဂ	-!- SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND SOME TO A GLUCAN-
38	BINDING PROTEIN FROM S.MUTANS.
ဂ္ဂ	This SWISS-PROT entry is copyright. It is produced through a collaboration
S	between the Swiss Institute of Bioinformatics and the EMBL outstation -
ဂ္ဂ	pean Bioinformatics Institute. There
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88	entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Matches 1
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P13470; P05427;
P13470; P05427;
O1-NOV-1988 (REL. 09, GREATED)
O1-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-SI PRECURSOR (EC 2.4 1.5) (GTE
EMBL; M22054; G153643; -. EMBL; M17361; G153641; -. PIR; JT0345; JT0345.
                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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"Sequence analysis of the 9tfB gene from Streptococcus mutans.";

"BACTERIOL. 169:4263-4270(1987).

"I BACTERIOL. 169:4263-4270(1987).

"I BACTERIOL. 109:4263-4270(1987).

"I BACTERION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

"I CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL) (N) -

"I SUBCELLULAR LOCATION: SECRETED.

"I SUBCELLULAR LOCATION: SECRETED.

"I DENTAL CARIES.
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UEDA S., SHIROZA T
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                                                                                                                                                                                                                                                                                                  SIMILARITY:
BINDING PROT
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larity 95.0%;
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                                                                                                                                                                                                                                                                                                  GLUCOSYLTRANSFERASES AND SOME TO A GLUCANS.
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Pred. No. 9.14e-13;
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CATALLTIC (APPROXIMATE).
GLUCAN-BINDING (APPROXIMATE).
A REPEAT.
A REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene from Streptococcus mutans GS-5.";
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                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1475;
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THE RESERVE OF SECOND SOCIOL SECOND S
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-: FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT OF PROCUTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT OF PROCUTION OF THE EXTRACES AND MEDIATE THE AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
-: CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) = D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).
-: SUBCELLULAR LOCATION: SECRETED.
-: SUBCELLULAR LOCATION: SECRETED.
-: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (REL. 11, CREATED)
01-JUL-1989 (REL. 11, LAST SEQUENCE UPDATE)
15-DEC-1998 (REL. 37, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-I PRECURSOR (EC 2.4.1.5)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
                                                                EMBL; M17391; G153647; -.
PFAM; PF00128; alpha-amylase; 1.
TRANSFERASE; GLYCOSYLTRANSFERASE;
                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE; 87308014.
FERRETTI J.J., GILPIN M.L., RUSSELL R.R.B.;
FERRETTI J.J. GILPIN M.L., RUSSELL R.R.B.;
Final and ide sequence of a glucosyltransferase
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                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produ between the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREPTOCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREPTOCOCCUS DOWNEI (STREPTOCOCCUS SOBRINUS).
BACTERIA; FIRMICUTES; BACILLUS/CLOSTRIDIUM GROUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
                                                                                                                                                                                                                                                                                                                                                                   GLUCANS.
SIMILARITY:
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GLUCAN-BINDING (APPROXIM
2.4 A, 1 C AND 1 AC REPEAT
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A REPEAT (INCOMPLETE).
MW; 3EA3727E CRC32;
                  RASE; SIGNAL; REPEAT; I POTENTIAL.
GLUCOSYLTRANSFERASE-I
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No. 9.54e-12;
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1 AC REPEATS.
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Best Local S
Matches 1
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                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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synthetase).";
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STREPTOCOCCUS DOWNEI (STREPTOCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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REPEAT
             TRANSFERASE; GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL SIGNAL 1 38 POTENTIAL.
                                                           PFAM; PF00128; alpha-amylase; HSSP; P00695; 2HEE.
                                                                                                     EMBL; D90213; G217033; -. PIR; A38175; A38175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-6715;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide sequences for sucrose splitting and glucan binding within streptococcus sobrinus glucosyltransferase (water-insoluble glucan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       554 VPSYSFAR-AHDSEVQDLI 571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACTERIOL. 173:989-996(1991).

- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECA OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.

CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N)

D-FRUCTOSE + (1,6-ALPHA-D-GLUCOSYL)(N+1).

SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                                                                                                                                                           SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES AND BINDING PROTEIN FROM S.MUTANS.
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GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH FORMS OF
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No. 9.56e-10;
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01-DEC-1992 (REL. 24, LAST SEQUENCE UPDATE)
01-APR-1993 (REL. 25, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5) (
SUCCOSSE 6-GLUCOSYLTRANSFERASE)
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                                                                                       EMBL; M30943; G153653; -. PIR; A41483; A41483.
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                                                             SIGNAL
                                                                     TRANSFERASE;
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                                                                               141483; A41483.
PF00128; alpha-amylase;
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16; Conser
                GLYCOSYLTRANSFERASE; SIGNAL; REPEAT; DENTAL CARIES.

1 36 OR 37 (POTENTIAL).

37 1365 GLUCOSYLTRANSFERASE-S.

37 1050 CATALYTIC (APPROXIMATE).

083 1365 GLUCAN-BINDING (APPROXIMATE).

083 1365 4.5 X TANDEM REPEATS.
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larity 84.2%;
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; BACILLUS/CLOSTRIDIUM GROUP;
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SOME TO A GLUCAN-
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01-FEB-1996 (REL. 33, CREATED)
01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
01-NOV-1997 (REL. 35, LAST ANNOTATION UPDATE)
GLUCOSYLTRANSFERASE-S PRECURSOR (EC 2.4.1.5)
(SUCROSE 6-GLUCOSYLTRANSFERASE).
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                                                                                SEQUENCE
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574 MANYIFIR-AHDSEVQTVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          e glucosyltransferase-S enzyme.";
GEN. MICROBIOL. 136:2099-2105(1990).
FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAL
OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIATE THE
AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
- CATALYTIC ACTIVITY: SUCROSE + (1,6-ALPHA-D-GLUCOSYL)(N) =
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                                                                                                                                                                                                                                                                                                                                        SIMILARITY: TO OTHER GLUCOSYLTRANSFERASES BINDING PROTEIN FROM S.MUTANS.
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SUBCELLULAR LOCATION: SECRETED.
                                                                                                                                                                                                      M29296; G153645; -
                                                                                                                                                                                          PF00128; alpha-amylase;
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                                       Similarity
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llarity 75.0%;
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CARBOHYD
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01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                             Local
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MITTED (JUN-1995) TO EMBL/GENBANK/DDBJ ABAKKS.
EUNCTION: NEUROPILAMENTS GSUALLY CONTAIN THREE IF PROTEINS: L. I
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER
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METAZOA; CHORDATA; VERTEBRATA; MAMMALIA; EUTHERIA;
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. 08, LAST SEQUENCE OF THE SEQU
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Pred. No. 4.
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   SEQUENCE FROM N.A.
MEDLITAR; 87282618.
NAPOLITANO E.W., CHIN S.S.M.,
"Complete amino acid sequence
                                                                                                                               01-CCT-1989 (REL. 12, CREATED)
01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NEUROPILAMENT TRIPLET M PROTEIN (160 KD NEU
                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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                                                                                      RATTUS NORVEGICUS (RAT).
EUKARYOTA; METAZOA; CHORDATA;
                                                                                                                    NEUROFILAMENT TRIPLET
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OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), TH
LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND
COLNCIDENT WITH A CHANGE IN THE NEUROFILAMENT FORMILY.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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PTM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P, NFM IS PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF: IT IS THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
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                                                                          MURIDAE;
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Pred. No. 2.12e-02
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GLYCOPROTEIN.
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SIMILARITY).
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                                                                          MAMMALIA;
RATTUS.
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   of rat NF-M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the middle molecular weight neurofilament protein."; J. NEUROSCI. 7:2590-2599(1987).
                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. I
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FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L,
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBEI
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                                                                                                                                                                                                                                                                                                       PF00038;
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             Similarity
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 Score 71; DB 1; I
Pred. No. 2.12e-02;
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01-APR-1988
01-AUG-1988
01-OCT-1996
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                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MYERS M.W., LAZZARINI R.A., LEE V.Y., SCHLAEPFER W.W., NELSON "The human mid-size neurofilament subunit: a repeated protein sequence and the relationship of its gene to the intermediate filament gene family."; EMBO J. 6:1617-1626(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NFM_HUMAN 
P07197;
                                                                                                                                                                                                                                 EMBL; Y00067; G35046; -. PIR; A27864; A27864. PIR; A30157; A30157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAZZARINI R.A.;
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01-AUG-1988 (REL. 08, LAST SCOUENCE UPDATE)
01-CCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEURO
    CARBOHYD
              CARBOHYD
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INIT_MET 0
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PROC. NATL. ACAD. SCI. U.S.A.
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EUKARYOTA; METAZOA; CHORDATA;
                           DOMAIN
                                     DOMAIN
                                                                                                                                                                                       INTERMEDIATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Identification of the
                                                                                                                                                                                                                                                                                                                                                                     PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FUNCTIONING OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY AND COINCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION: SIMILARITY: BELONGS TO THE INTERNEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: NEUROFILAMENTS USUALLY CONTAÎN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
PTM: THERE ARE A NUMBER OF REPEARTS OF THE TRIPEPTIDE K-S-P, NEW 15
PHOSPHORYLAGED ON A NUMBER OF THE SERINES IN THIS MOTIF. IT IS
THOUGHT THAT PHOSPHORYLATION OF NFH RESULTS IN THE FORMATION OF
INTERFILAMENT CROSS BRIDGES THAT ARE IMPORTANT IN THE MAINTENANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   OF AXONAL CALIBER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTVOS L. JR., CARDEN M.J., HOLLOSI M., DIETZSCHOLD
                                                                                                                                                                                     FILAMENT; HEPTAD REPEAT PATTERN; COILED COIL; NEURONE;
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HEPTAD RAB;
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D REPEATS.
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C (BY SIMILARITY).
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           AINX_RAT
P23565;
01-NOV-1991
01-OCT-1996
15-JUL-1998
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01-NOV-1995 (REL. 3
01-FEB-1996 (REL. 3
ALPHA-INTERNEXIN (A
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01-NOV-1995
01-FEB-1996
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P46660;
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01-NOV-1991 (REL. 20, CREATED
01-OCT-1996 (REL. 34, LAST SE
15-JUL-1998 (REL. 36, LAST AN
ALPHA-INTERNEXIN (ALPHA-INX).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intermediate filament protein alpha-internexin.";
GENE 149:289-292(1994).
-i- FUNCTION: CLASS-IV NEURONAL INTERMEDIATE FILAMENT.
-i- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
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SEQUENCE FROM N.A.
SEQUENCE FROM TISSUE-SPLEEN;
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EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; MAMMALIA;
RODENTIA; SCIUROGNATHI; MURIDAE; MURINAE; MUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute.
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TE; PS00256; IF; 1.
PF00038; filament; 1.
PF00038; filament; HEPTAD RE.
1 87 ROD.
88 408 ROD.
409 504 TAIL.
409 504 TAIL.
409 504 TAIL.
238 TAIL.
238 TAIL.
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32, LAST SEQUENCE UP
33, LAST ANNOTATION
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36, LAST ANNOTATION UPDATE
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Pred. No.
5; Misma
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POLY-GLU.
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                                                                     PRT;
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EMBL; M73049; G204964; -...
PIR; S12379; S12379;
PROSITE; PS00226; IF; 1.
PFAM; PF00038; filament; 1
INTERMEDIATE FILAMENT; HEP
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Q03571;
Q1-FEB-1994
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or send a
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MEDLINE; 92011743.

CHING G.Y., LIEM R.K.H.;

CHING G.Y., LIEM R.K.H.;

"Structure of the gene for the neuronal intermediate filament pr
alpha-internexin and functional analysis of its promoter.";

J. BIOL. CHEM. 266:19459-19468(1991).

-i- FUNCTION: CLASS-UBURONAL INTERMEDIATE FILAMENT.

-i- DEVELOPMENTAL STAGE: LEVELS OF THIS PROTEIN REACH A MAXIMUM
EMBRYONIC DAY 16 AND DECLINE INTO ADULTHOOD.

-i- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                         CAENORHABDITIS ELEGANS.
EUKARYOTA; METAZOA; NEMATODA; SECERNENTEA; RHABDITIA; RHABDITIDA;
                                                                                                                        01-FEB-1994
01-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                HYPOTHETICAL C40H1.1.
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                       RHABDITINA;
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novel neuronal intermediate
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ediate filament protein.";
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BRAIN RES. 387:243-250(1986).

- FUNCTION: NEUGOFILAMENTS USUALLY CONTAIN THREE IF PROTEINS:
- FUNCTION: NEUGOFILAMENTS USUALLY CONTAIN THREE IF PROTEINS:
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- THOUGHT THAT PHOSPHORYLATION OF NEH RESULTS IN THE FORMATION
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MUS MUSCULUS (MOUSE).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                          LEVY E., LIEM R.K.H., D'EUSTACHIO P., COWAN N.J.;
"Structure and evolutionary origin of the gene encoding mouse NF-M,
the middle-molecular-mass neurofilament protein.";
EUR. J. BIOCHEM. 166:71-77(1987).
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OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE LEVELS OF PHOSSHORYLATION BEING ALTERED DEVELOPMENTALLY AND CONCIDENT WITH A CHANGE IN THE NEUROFILAMENT FUNCTION.
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.

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OF AXONAL CALIBER.

OF THE LARGER NEUROFILAMENT POLYPEPTIDES (NF-M AND NF-H), THE

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SECOPT D., DINEVA B., BETZ H., GUNDELFINGER E.D.;
"ISOlation of the chicken middle-molecular weight neurofilament (NF-M) gene and characterization of its promoter.";
(NF-M) gene and characterization of its promoter.";
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                                     SEQUENCE OF 259-857 FROM N. MEDLINE; 88112814.
                                                                                                                                                                                                                                 NEOGNATHAE;
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     OPF D., HERMAN
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ONIT_MET 0
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                     HERMANS - BORGMEYER
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                                                                                                                                                                                                                                 GALLIFORMES;
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FILAMENT; HEPT
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14, LAST SEQUENCE UPDATE)
34, LAST ANNOTATION UPDATE)
PLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).
 gene
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LINKER 2.
COIL 2B.
GLCNAC (BY SIMILARITY).
GLCNAC (BY SIMILARITY).
GLCNAC (BY SIMILARITY).
S -> F (IN REF. 2).
QA -> RR (IN REF. 2).
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Pred. No. 1.39e-01;
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COIL 1B.
LINKER 12.
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ROD.
TAIL.
COIL 1A.
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GUNDELFINGER
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developing
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Search completed: Tue Jan Job time: 8 secs.

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SFIRTAHDSEVODLIA

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                     Matches
                               Query Match
Best Local
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CARBOHYD
CONFLICT
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DOMAIN
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                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                            INTERMEDIATE
226 AFLRGNHEEEVAELLA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: NEUROFILAMENTS USUALLY CONTAIN THREE IF PROTEINS:
AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALL
PIM: THERE ARE A NUMBER OF REPEATS OF THE TRIPEPTIDE K-S-P.
PHOSPHORYLATED ON A NUMBER OF THE SERINES IN THIS MOTIF: IT
                                                                                                                                                                                                                                                                                                                                                                                                                                        PTM: PHOSPHORYLATION SEEMS TO PLAY A MAJOR ROLE IN THE FOF THE LARGER NEUROPILAMENT POLYPEPTIDES (NE'M AND NE'H) LEVELS OF PHOSPHORYLATION BEING ALTERED DEVELOPMENTALLY COINCIDENT WITH A CHANGE IN THE NEUROPILAMENT FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THOUGHT THAT PHOSPHORYLATION OF NFH R INTERFILAMENT CROSS BRIDGES THAT ARE OF AXONAL CALIBER.
                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
                                                                                                                                                                                                                                                                          A27040; A27040
S08061; S08061
S15762; S15762
                                                                                                                                                                                                                                                                                                         X17102; G63689; -.
X05558; G63686; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system: characterization
                                Similarity
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                                                                                                                                                                                                                                            8; filament;
FILAMENT; H
                     Conservative
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                                                                                                                                                                                                                                GLYCOPROTEIN.
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                              49.6%;
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857
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HEPTAD REPEAT PATTERN; COILED COIL; NEURONE;
                                                                WW;
                     Pred.
                                        Score 67;
                                                                         COIL 1B.
LINKER 12.
COIL 2A.
LINKER 2.
COIL 2B.
GLCNAC (BY
GLCNAC (BY
G -> R (IN
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LINKER 1.
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                     Mismatches
                              67; DB 1; I
No. 1.39e-01;
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(BY
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                                                                        Y SIMILARITY).
Y SIMILARITY).
N REF. 2).
                                                               CRC32;
                                        Length 857;
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                     Indels
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(ME)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:36:00 2000; MasPar time 5.50 Seconds
81.178 Million cell updates/sec

ar output not generated.

Title: >US-09-290-049-1
Description: (1-21) from US09290049.pep
Perfect Score: 148

1 ANDHLSILEAWSDNDTPYLHD 21

Sequence:

Scoring table: PAM 150 Gap 15

med: 170751 seqs, 21266608 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-geneseq35

1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13 14:part14 15:part15 16:part16 17:part17 18:part18 19:part19 20:part20 21:part21 22:part22 23:part23 24:part24 25:part25 26:part26 27:part27 28:part28 29:part29 30:part30 31:part31 32:part32 33:part33 34:part34 35:part35 36:part36 37:part37 38:part38 39:part39

Statistics: Mean 20.949; Variance 72.779; scale 0.288

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	14	13	12	11	10	· w	æ	7	6	G	4	ω	2	. بـــ	Result No.
62	62	62	62	62	62	62	62	62	62	62	63	66	83	131	Score
41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	41.9	42.6	44.6	56.1	88.5	Query Match
	648	648	648	648	648	648				648 2	388		1577	1592	Query Match Length DB
32	22	21	4	4	4	4	22	22	22	22	ü	33	6	0	. B
W17049 W62220	W17048	W13107	R25277	R22561	R22562	R22560	W17047	W17046	W17044	W17045	W62298	W62297	R91047	R32925	ID
Mutant mouse c-raf 1 Raf-1 protein.	Mutant mouse c-raf 1	Human Raf-1.	Human c-raf-1.	٠.	Mouse mutant c-raf-1.	Mouse mutant c-raf-1.	Mutant mouse c-raf 1	Mutant mouse c-raf 1	_	Mouse c-raf 1 protein	Wheat D1 protease.	Scenedesmus D1 protea	Alpha-D-glucosyltrans	Glucosyltransferease	Description
6.43e+01 6.43e+01	6.43e+01	6.43e+01	6.43e+01	6.43e+01	6.43e+01	6.43e+01	6.43e+01	6.43e+01	6.43e+01	6.43e+01	5.20e+01	2.73e+01	6.09e-01	5.55e-06	Pred. No.

RESULT ID R

T 2: R91047 standard; Protein; 1577 AA. Š

Query Match 88.5%; Best Local Similarity 85.7%; Matches 18; Conservative

Score 131; DB 6; L Pred. No. 5.55e-06; 3; Mismatches 0;

Length 1592; ; 0; Indels

0

Gaps

0

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19.	18	17
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30	29	35	15	<u>, , , , , , , , , , , , , , , , , , , </u>	N	رح.	w	20	14	39	14	9	14	28	H	3	39	17	12	_	ü	34	38	3 8	ω	18	4	4
572	W55287	456	049	292	029	R25385	437	9	861	W67891	861	790	R78615	549	677	831	136	R85891	596	900	230	148	993	002	561	821	R22559	256
98e10	H. pylori ORF 13ep120	a albicans oli	н	dus		Factor XIII.	r XIII subunit	Factor XIIIa	ion vector pM	sec	٠	ne programmed ce	extracellular	argeting ligand d	binding per	ylococcus au	엺	D-40		c gamma rece	1 pr	cobacter polype	igen 1 from c	xpressed anti	ha 2 ma	kinas	Mouse c-raf-1.	Mouse mutant c-raf-1.
.83e+0	.83e+0	.49e	.49e+0	.49e+0	.49e	.49e+0	.49e	9e+0	.49	.49e+0	.49e+0	.49e	.49e+0		.49e+0	٠.	.21e+0	.21e	.21e+0	.21e+0	.81e+0	.81e+0	9.81e+0	9.81e+0	9.81e+0	6.43e+0	.43e+0	6.43e+01

ALIGNMENTS

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RESULT
                  Claim 13; Page 15; 29pp; Japanese.

The DNA sequence from Streptococcus sobrinus strain 6715 encodes glucosyltransferase-I (and mutants). The DNA was obtd. by treating 5. sobrinus 6715 with mutanolysin, extracting the chromosomal DNA, partially digesting with Sau3AI and fractionating on agarose gel. The 3-5 kbp fragment was ligated into pUC18 and E. coli JM109 transformed with it. A GT-I expressing clone was isolated and sequenced. The clone may be used in the development of a drug for
                                                                                                                                                                                                                                                                                                                                                                Glucosyltransferease I.
GT-1; Streptococcus; dental; caries.
                                                                                                                                                                                                                                                                                                                                                                                                 R32925 standard; Protein; 1592
R32925;
28-JUN-1993 (first entry)
dental caries.
Sequence 159
                                                                                                                                                                             DNA sequence glucosyl:transferase-I - comprises Streptococcus sobring DNA sequence with at least one nucleotide added or
                                                                                                                                                                                                                                                                                                                                                 Streptococcus sobrinus.
                                                                                                                                                                                                                N-PSDB; Q37760.
                                                                                                                                                                                                                              (KATO/) KATO K.
WPI; 93-079449/10.
                                                                                                                                                               deleted
                                                                                                                                                                                                                                                                                   25-JUL-1991;
                                                                                                                                                                                                                                                                                                                  02-FEB-199
                                                                                                                                                                                                                                                                (FUKU/) FUKUI
 1592 AA;
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Best Local
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activity

Claim 23; Page 44-45; 73pp; English.

Claim 23; Page 44-45; 73pp; English.

A method has been developed for identifying a herbicidal agent which
A method has been developed for identifying a incubating a Di protease
inhibits Di protease. The method comprises: (a) incubating a Di protease
enzyme in a sample suspected of containing a herbicidal agent with a
enzyme in a sample suspected of containing a herbicidal agent with a
suitable Di enzyme substrate, where an enzyme product is formed; and (b)
suitable Di enzyme substrate, where an enzyme product of step (a). Also described
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JIT 3
W62297 standard;
W62297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alpha-D-glucosyltransferase.

Alpha-D-glucosyltransferase, primer-independent; soluble glucan;

sucrose; transgenic plant; cloning; Escherichia coli;

phage lambda-Cl3; vector; plasmid pGSG501; plasmid pGSG502;

gene transfer; crop improvement; storage carbohydrate; pasture;

feedstuff; senescence; dextran; binder; food; pharmaceutical.

Streptococcus salivarius strain ATCC 25975.

WOSGO173-Al.
                                                                                                                                                                                                                                                               11-JUN-1998.
03-DEC-1997; U21964.
05-DEC-1996; US-759581.
05-DEC-1996; US-759581.
CDUPO ) DU PONT DE NEMOURS & CO E I.
(DUPO ) DU PONT BA, DONALdSON GK,
JORDAN DB, Tang XS, Trost JT, Wang S,
WPI: 98-333349/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scenedesmus D1 protease: Scenedesmus; D1 protease; herbicide; inhibition; alga; wheat; detection; identification.
                                                                                                                                                                                          New isolated plant DI protease(s) agents which target the DI proteas
                                                                                                                                                                                                                                              N-PSDB; V39818
                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9824934-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scenedesmus obliquus
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22-MAY-1996
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nes 13; Conser
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72.2%;
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                                                                                                                                                                                          used for identifying herbicidal by inhibiting the enzyme
                                                                                                                                                                                                                                                                                          Hershey
, Warren
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6.09e-01;
---hes 5;
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                                                         Conditions to permit D1 turnover; and (c) measuring the variable CC conditions to permit D1 turnover; and (c) suspected herbicidal agent which a crosspected herbicidal agent with a sample suspected of containing a herbicidal agent with a constant of the present invention are; (1) a method for detecting in vivo a content of the present invention are; (1) a method for detecting in vivo a content of the present invention are; (1) a wild type cell comprising; (a) preparing a content of mixture comprising; (i) a wild type cell comprising an active D1 core complex capable of processing a D1 protease; and a photosystem conditions to permit D1 turnover; and (c) measuring the variable conditions to permit D1 turnover; and (c) measuring the variable controphyll fluorescence enzyme conditions to permit D1 turnover; and (c) measuring the variable controphyll fluorescence correlates with herbicidal activity of the suspected herbicidal agent; (2) a gene encoding a D1 protease enzyme collated from; (a) wheat; (b) tobacco; (c) spinach; (d) Scenedesmus; or conspectively). Native or recombinant D1 proteases can be used to develop contributions control detection of herbicidal compositions capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the present invention are: (1) a method for detecting in vivo a C herbicidal agent which inhibits D1 protease comprising: (a) preparing a C reaction mixture comprising: (1) a wild type cell comprising an active D1 protease enzyme capable of processing a D1 pre-protein; and a Photosystem CC II core complex capable of processing a D1 protease; and (iii) suitable CC suspected herbicidal agent which inhibits D1 protease; and (iii) suitable CC growth medium; (b) illuminating the reaction mixture at illumination CC conditions to permit D1 turnover; and (c) measuring the variable CC chlorophyl1 fluorescence produced in step (b), where the level of the conditions to permit D1 turnover; and (c) measuring the variable CC variable chlorophyl1 fluorescence correlates with herbicidal activity of the suspected herbicidal agent; (2) a gene encoding a D1 protease enzyme CC isolated from: (a) wheat; (b) tobacco; (c) spinach; (d) Scenedesmus; or CC isolated from: (a) wheat; (b) tobacco; (c) spinach; (d) Scenedesmus; or CC (e) Synechocystis; (see v39818 to v39822, which encode w62297 to w62301 crespectively). Native or recombinant D1 proteases can be used to develop continued the control of herbicidal compositions capable of
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03-DEC-1997.
05-DEC-1996; US-759581.
05-DEC-1996; US-759581.
(DUPO) DU PONIT DE NEMOURS & CO E I.
Chisholm DA, Diner BA, Donaldson GK, He
Jordan DB, Tang XS, Trost JT, Wang S, W
WPI; 98-333349/29.
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Triticum sp
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Similarity 36.8%;
7; Conservative
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Pred. No. 2.73e+01;
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Query Match Best Local Similarity

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26 AUG-1988; 236947.
26-AUG-1988; US-236947.
16-SEP-1991; US-759738.
24-JAN-1994; US-185282.
(USSH) US DEPT HEALTH 6
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26-AUG-1988; 236947.
26-AUG-1988; US-236947.
26-AUG-1998; US-236947.
16-SEP-1991; US-759738.
24-JAN-1994; US-185282.
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W17044 standard; F
W17044;
07-JUL-1997 (firs
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Example 3; Column 11-14; 26pp; English.
W17045, the mouse c-raf-1 protein, was used in a method for classifying a lymphoma or lung cancer. The normal sequence given here was compared with the sequence of c-raf 1 proteins derived from different tumours indice. The method, when used for diagnosing human tumours, involves detecting the presence of a point mutation in a conserved region of the c-raf-1 gene (codon 53), encoding Ser, in this sequence) derived from lymphoma or lung cancer tissue and classifying the lymphoma or lung cancer as a c-raf-1 mutation-associated cancer if one or more point mutations are present. The method is particularly applicable to lung
Classification of lymphoma or lung cancer - on the basis of a point mutation in c-raf-1 gene claim 2; Column 35-38; 26pp; English.
W17044, the human c-raf-1 protein, was used in a method for classifying a lymphoma or lung cancer in an individual. The method involves detectif the presence of a point mutation in a conserved region of the c-raf-1
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Rapp UR, Storm SM;
WPI; 97-225421/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human c-raf 1 protein used in diagnosis of lymphoma or lung cancer. raf; oncogene; lymphoma; lung cancer; neoplasia; point mutation; conserved region; adenocarcinoma; codon 533; diagnosis; detection.
                                                                                                                                                                                                              Rapp UR, Storm SM; WPI; 97-225421/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
US5618670-A.
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lymphoma; lung cancer; neoplasia; point mutation;
on; adenocarcinoma; codon 533; diagnosis; detection.
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26-AUG-1988; US-236947.
16-SEP-1991; US-759738.
24-JAN-1994; US-185282.
                                                                                     26-AUG-1988; 236947.
26-AUG-1988; US-236947.
16-SEP-1991; US-759738.
24-JAN-1994; US-185282.
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Example 3; Column 13-18; 26pp; English.

MJ7046-WJ7049 are mutant versions of the mouse c-raf-1 protein, derived from four different types of tumour. They were used in a method for classifying a lymphoma or lung cancer, by comparison with the wild-type c-raf 1 protein sequence derived from different tumours in mice. The method, when used for diagnosing human tumours, involves detecting the presence of a point mutation in a conserved region of the c-raf-1 gene (codon 533, encoding Ser) derived from lymphoma or lung cancer tissue and classifying the lymphoma or lung cancer as a c-raf-1 mutation-associated cancer if one or more point mutations are present. The method is particularly applicable to diagnosis of lung adenocarcinoma.
Rapp
WPI;
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16-JUL-1997 (first entry)
Mutant mouse c-raf 1 protein used in diagnosis of cancer.
raf; oncogene; lymphoma; lung cancer; neoplasia; point mutation;
raf; oncogene; adenocarcinoma; codon 533; diagnosis; detection
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W17047 standard; Protein;
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16-SEP-1991; 759738.

16-SEP-1991; US-759738.

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Detecting C-RAF-1 genes -

analysing prods. and clas
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                                                                                                                                                                                                                                                      Disclosure; Page 28; 65pp; English.

The sequence is that of a mutated version of mouse c-raf-1, the mutation occurs just downstream of the APE site, the mutation not artifactual. The region in which it occurs overlaps an epi shared by monoclonal antibodies generated against raf (Kolch e 1990). This region is a hydrophilic domain, the structure of w is predicted to be altered by this mutation.

See also R25277 and R22559-R22563.

Sequence 648 AA;
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25-FEB-1992: 759738.
16-SEP-1991: US-236947.
26-AUG-1988: US-236947.
16-SEP-1991: US-759738.
(USSH ) US DEPT HEALTH & Rapp U, Storm S;
WPI: 92-123681/15.
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WPI; 92-123681/15
Detecting C-RAF-1 genes
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26-AUG-1988; US-236947.
16-SEP-1991; US-759738.
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513..5
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classifying individual having mutation(s)
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25-FEB-1992.
16-SEP-1991; 759738.
26-AUG-1988; US-236947.
16-SEP-1991; US-759738.
                                                                                                                                                                                                                                                                                                                           Disclosure: Page 46; 65pp; English.

The sequence is that of human c-raf-1, the c-raf-1 gene can be used in methods for detecting and treating a wide range of cancers including lung cancer, T-cell lymphomas, renal cell carcinoma, ovarian carcinoma and mixed parotid gland tumours. The methods consist of amplifying the gene by PCR and then, based on the presence or absence of one or more mutations, individuals at increased risk can be detected and prognosis and treatment determined. See also R22559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ET 12
R25277 standard; Protein; 648
R25277;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 31; 65pp; English.

The sequence is that of a mutated version of mouse c-raf-1, the mutation occurs just downstream of the APE site, the mutation is not artifactual. The region in which it occurs overlaps an epitope shared by monoclonal antibodies generated against raf (Roich et al. 1990). This region is a hydrophilic domain, the structure of which is predicted to be altered by this mutation.

See also R25277 and R22559-R22563.
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                                                                             Human; raf-1; complex; 14-3-3; beta; detection; screening; interaction; co
                                                                                                          Human Raf-1
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W13107;
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WPI; 92-123681/15.
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/note= "conserved region
186..332
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and classifying individual having mutation(s) in
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Mismatches 7;
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No. 6.43e+01;
                                                                             a; zeta; modulation; binding;
cell cycle; control; neoplasia;
           1 containing region"
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                                                                                                                                                                                                                          PR Classification of lymphoma or lung cancer - on the basis of a point of Classification of lymphoma or lung cancer - on the basis of a point mutation in c-raf-1 gene Example 3; Column 21-24; 26pp; English.

CC W17046-W17049 are mutant versions of the mouse c-raf-1 protein, derived from four different types of tumour. They were used in a method for classifying a lymphoma or lung cancer, by comparison with the wild-type CC craf 1 protein sequence derived from different tumours in mice. The method, when used for diagnosing human tumours, involves detecting the CC presence of a point mutation in a conserved region of the c-raf-1 gene CC codon 533, encoding Ser) derived from lymphoma or lung cancer tissue associated cancer if one or more point mutations are present. The method is particularly applicable to diagnosis of lung adenocarcinoma.
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Best Local Similarity 30.0%;
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Best Local :
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26-AUG-1988; 236947.
26-AUG-1988; US-236947.
16-SEP-1991; US-759738.
24-JAN-1994; US-185282.
(USSH.) US DEPT HEALTH & HUMAN SI
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14-JUL-1994; US-276151.
(ONYX-) ONYX PHARM INC.
Freed E, Ruggleri R;
WPI; 97-108327/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure: Columns 31-38; 43pp; English.

The present sequence is human Raf-1, which can be used in a novel composition comprising a complex of human Raf-1, or a fragment comprising residues 1-197 or 186-332, or lacking residues 51-131, and a 14-3-3 polypeptide (preferably human 14-3-3 beta or zeta). The composition can be used to screen for drugs which modulate the binding interaction between Raf-1 and 14-3-3, especially to identify drugs that modulate Raf-1 mediated cell cycle control, and/or neoplastic or other pathological conditions dependent on the interaction between Raf-1 and 14-3-3 beta or zeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rapp UR,
WPI; 97-2
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W17048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant mouse c-raf 1 protein used in diagnosis of cancer. raf; oncogene; lymphoma; lung cancer; neoplasia; point mutation; conserved region; adenocarcinoma; codon 533; diagnosis; detection.
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Complex of raf-1 and 14-3-3 polypeptide(s)
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1 ANDHLSILEAWSDNDTPYLH
                                                   tkdnlaivtqwcegsslykh
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DE NIT7049 standard; Protein; 648 AA.

AC MI7049

AC MI7049

DT 16-UUL-1997 (first entry)

DE Mutant mouse craf | protein used in diagnosis of cancer.

KW conserved region; adenocarcinoma; codon 533; diagnosis; detection.

KW conserved region; adenocarcinoma; codon 533; diagnosis; detection.

SW US5618670-A.

PR 26-ANG-1988; US-236947.

PR 26-ANG-1988; US-759738.

PR 24-JAN-1994; US-759738.

PR 29-1991; US-759738.

PR 24-JAN-1994; US-759738.

PR 25-AUG-1988; US-25641/20.

PR 24-JAN-1994; US-758738.

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Release 3.1A John F. Collins, Biocomputing Research Unit. Copyright (c) 1993-1998 University of Edinburgh, U.K. Distribution rights by Oxford Molecular Ltd

MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Jan 11 15:38:57 2000; MasPar time 1.65 Seconds 151.295 Million cell updates/sec

ar output not generated.

Description: Perfect Score: Sequence: >US-09-290-049-1 (1-21) from US09290049.pep 148 1 ANDHLSILEAWSDNDTPYLHD 21

Scoring table: PAM 150 Gap 15

Searched: 122461 seqs, 11912985 residues

Post-processing: Minimum Match 0% Listing first 45 summaries

Database: a-issued 1:5A_COMB 2:5B_COMB 3:PCT9_COMB 4:backfiles1

Statistics: Mean 19.740; Variance 68.890; scale 0.287

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	4.	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	
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÷	1.63e+02	1.63e+02	1.63e+02	1.63e+02	1.63e+02	1.33e+02	1.33e+02	1.33e+02	1.33e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	1.08e+02	8.72e+01	8.72e+01	

ALIGNMENTS

888888888888888	88888888888	###88888888888888888888888888888888888	RESULT ID U XX AC x XX DT
OPERATING SYSTEM: MICROSOFT WINDOW SOFTWARE: MICROSOFT WORD 2.0C CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/759,581B FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: FLOYD, LINDA AXAMETHY REGISTRATION NUMBER: 33,692 REFERENCE/DOCKET NUMBER: CR-9964 TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-8112 TELEPAX: 302-773-0164 INFORMATION FOR SEQ ID NO: 4:	NUMBER OF SEQUENCES: 29 CORRESPONDENCE ADDRESS: ADDRESSE: E.I. DU PONT DE N STREET: 1007 MARKET STREET CITY: WILMINGTON STATE: DELAWARE COUNTRY: U.S.A: LIP: 19898 COMPUTER READABLE FORM: MEDIUM TYPE: DISKETTE, 3.50 COMPUTER: IBM PC COMPATIBLE	pplication US 876945 876945 CHISHOLM, CHISHOLM, CHISHOLM, HERSHEY, H DONALDSON, HERSHEY, F JORDAN, DC TANG, XIAG TANG, XI	7 1 US-08-759-581B-4 STANDARD; XXXXXX
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                                                               INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
MOLECULE TYPE: MW; 1062471 CN;
JENCE 464 AA; 48755 MW; 1062471 CN;
                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT W
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
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MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETT
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ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
                                                      SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
                                                                      TELEFAX:
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                                      TYPE: amino acid
                                                                              TELEPHONE:
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                                                                                                                                                                                                                  WILMINGTON : DELAWARE
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    Application US/08759581B
5876945

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INVENTION: METHODS FOR IDENTIFYINGHERBICIDAL AGENTS THAT INHIBIT D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                               DONALDSON, GAIL K.
HERSHEY, HOWARD P.
JORDAN, DOUGLAS B.
TANG, XIAO-SONG
TROST, JEFFREY T.
WANG, SHAOJIE
                                              464 amino acids
                                                                      : 302-892-8112
302-773-0164
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                                                                                                                                            US/08/759,581B
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Pred. No. 1.25e+01;
7; Mismatches 5
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                                                                                             CR-9964
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                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.
ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INC
COMPUTER: IBM FC COMPATIBLE
COMPUTER: HIM MICROSOFT WIN
SOFTWARE: MICROSOFT WORD 2.0C
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                        TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
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                                                                      MOLECULE TYPE:
ORIGINAL SOURCE:
STRAIN: WHEAT
                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: E.I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 388 amino acids
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: METHODS FOR IDENTIFYINGHERBICIDAL AGENTS THAT INHIBIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                   TOPOLOGY:
                                                                                                                              TYPE: amino acid
STRANDEDNESS: un
                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
 Similarity 38.9% 7; Conservative
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                                                          388
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HERSHEY, HOWARD P.
JORDAN, DOUGLAS B.
TANG, XIAO-SONG
TROST, JEFFREY T.
WANG, SHAOJIE
                                                          Ą,
                                                         WHEAT D1 PROTEASE PROTEIN AA; 41958 MW; 750252 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WARREN, PATRICK V.
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                42.6%;
38.9%;
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Pred. No. 1.
7; Mismatc
Score 63; DB 2; L
Pred. No. 2.41e+01;
6; Mismatches 5
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1.25e+01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Benner
                                                              68 TKDNLAIVTQWCEGSSLYKH 87
                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                \vdash
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/857,224B
FILING DATE: 03/25/92
                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                 MOLECULE TYPE:
DESCRIPTION: protein
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: none TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                            PUBLICATION INFORMATION:
                                              ANDHLSILEAWSDNDTPYLH
                                                                                                                                                      TITLE: THE JOURNAL: VOLUME:
                                                                                                                                              PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple MacIntosh OPERATING SYSTEM: MacInto
                                                                                                                                       DATE:
                                                                                                                                                                                               AUTHORS: Hanks, S. K. AUTHORS: Quinn, A. M.
                                                                                                                                                                                                                 AUTHORS:
                                                                                                                                                                                                                                     ORGANISM: Saccharomyces cerevisiae
ATURE: Protein kinase; Table 8 Column
                                                                                                                                                                                                                                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                         LENGTH:
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267 AA; 30518 MW; 382200 CN;
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                                                                                      Conservative
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                                                                                                                                                                          The protein kinase family
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(International) 41 1 262 2437
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                                                                                               41.9%;
         STANDARD;
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Predicting Folded Structures of Proteins
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Pred. No. 3.00e+01;
7; Mismatches 7;
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          PRT;
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         315 AA
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Best Local S
Matches
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                                                                                                                                                                                                                                                                SEQUENCE
                                                                        Sequence 12, Application US/08909983
                                                                                                                                    US-08-909-983-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12, Application US/08909984A
                              Patent No. 5747288
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08909984A Patent No. 5747275
                                                   Sequence 12,
                                                                                                                                                                                                 80 TKDNLAIVTOWCEGSSLYKH 99
                                                                                                                                                                                                                              Match 41.9%;
Local Similarity 30.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: A NO. 3/4/2...
TITLE OF INVENTION: Signal Transduction
TITLE OF INVENTION: 12
                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
JENCE 315 AA; 35949 MW; 526392 CN;
                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: B9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acid
            APPLICANT:
   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: not
TOPOLOGY: not red
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                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                   Application
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(415) عد
Rubin, Gerry M.
Therrien, Marc
Chang, Henry C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                  not relevant
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                                                   US/08909983
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                                                                                                                                                                                                                                                                    Sequence 12, Application US/08571758 Patent No. 5700675
                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/571,758
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B96-010
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Rubin, Gerry M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80 TKDNLAIVTQWCEGSSLYKH 99
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TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 12:
APPLICANT: Chang, Henry C.
APPLICANT: Karim, Felix D.
APPLICANT: Wassarman, David A.
APPLICANT: Wassarman, David A.
TITLE OF INVENTION: A NO. 5700675el Protein Kinase Required for INTLE OF INVENTION: Signal Transduction
NUMBER OF SEQUENCES: 12
CORRESPONDENCES: 12
CORRESPONDENCE A TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS: LENGTH: 315 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/909,983 FILING DATE: 12-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A NO. 5747288el Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANDHLSILEAWSDNDTPYLH
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TOPOLOGY: not
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315 AA; 35949 MW; 526392 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: B96-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 315 amino acids
                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08276151
        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNUMBER: US/08/276,151
FILING DATE: 14-JUL-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TOICHIA, Ph.D., Timothy E
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                     Patent No. 5597719
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                            Sequence 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 TKDNLAIVTOWCEGSSLYKH
                                                                                                                                                                                                                                                                                                                                                                                                                              1 ANDHLSILEAWSDNDTPYLH
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward et al.
STREET: Five Palo ALto Square
                                                                                                                                                                                                                     APPLICANT: Freed, Ellen
APPLICANT: Ruggleri, Rosamaria
TITLE OF INVENTION: Interaction of
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/571,758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: not relevant
                                                                                                                                               COUNTRY: U
ZIP: 94036
                                                                                                                                                                   STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JE TYPE: peptide
315 AA; 35949 MW; 526392 CN;
                                                                                                                                                                                                                                                                                   , Application US/08276151 
5597719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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Pred. No.
ONYX-005/00US
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                                                                                                                                                                                                                                     raf-1 and 14-3-3 Proteins
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Best Local Similarity 30.0%; Pred. No.
Matches 6; Conservative 7; Misma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/08185282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     111 TKDNLAIVTQWCEGSSLYKH 130
                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 857-0663
INFORMATION FOR SEQ ID NO: 5:
                                                     TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                     SEQUENCE CHARACTERISTICS LENGTH: 648 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linea MOLECULE TYPE: po HYPOTHETICAL: NO
                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 346 amino acid
LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                    TELEPHONE: (202) 861-3000
                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rapp, Ulf R. APPLICANT: Storm, Stephen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 843-5481
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                                                                                                         NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                   STREET: 1615 L St
CITY: Washington
                                                                        TELEFAX:
                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   346 AA; 39386 MW; 635811 CN;
                                                                                                                                                                                                                                                                                                                                                                                                                      2, Application US/08185282
5618670
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                                                                                                                                                                                                                              Release #1.0, Version #1.25
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                                                                                                                    26,581
                                                                                                          WTS/5683/82732
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413 TKDNLAIVTOWCEGSSLYKH 432
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Local Similarity 30.0%;
                     Local Similarity les 6; Conser
                                                                                                                                                                                         TELEFAX: (404) 818-3799 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Young, Leona G.
REGISTRATION NUMBER: 37,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yoo, Tai-June
APPLICANT: Cheng, Kuang-Chuan
TITLE OF INVENTION: Autoimmune Inner Ear Disease
TITLE OF INVENTION: Diagnostic Assay
                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (404) 818-3700
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                         ANTI-SENSE:
                                                                                                                  HYPOTHETICAL:
                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 191 PO
                                                                        ORGANISM:
                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                   STATE: Georgia COUNTRY: U.S.A.
                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                             VISM: Homo sapiens 648 AA; 73051 MW;
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Conservative
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                                                                                              N-terminal
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                     Pred.
                          Score 62; DB 2; pred. No. 3.00e+01
                                                                                                                                                                                                                                             37,266
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Pred. No. 3.00e+01;
                                                              2254837 CN;
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CORRESPONDENCE ADDRESS:

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                                                           Sequence 3, Application US/08185282
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                                                                                                                                                    413 TKDNLAIVTQWCEGSSLYKH 432
                                      Sequence 3, Application US/08185282 Patent No. 5618670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08276151 Patent No. 5597719
GENERAL INFORMATION:
APPLICANT: Rapp, Ulf R.
APPLICANT: Storm, Stephen M.
TITLE OF INVENTION: DETECTIONUMBER OF SEQUENCES: 12
                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                            TELEFAX: (415) 857-06
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                      1 ANDHLSILEAWSDNDTPYLH
                                                                                                                                                                                                                                                        NAME: TOTCHIA, Ph.D., Timoti REGISTRATION NUMBER: 36,700 REFERENCE/DOCKET NUMBER: ON TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 843-5481
                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              FILING DATE: 14-JUL-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 14-JUL-19
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward et al.
STREET: Five Palo ALto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Freed, Ellen
APPLICANT: Ruggieri, Rosamaria
TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
                                                                                                                                                                                                MOLECULE TYPE: protein
MENCE 648 AA; 73051 MW; 2254837 CN;
                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                               TYPE: ami
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                                                                                                                                                                                                                linear
                                                                                                                                                                           41.98;
                                                                                                         STANDARD;
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, 857-0663
 DETECTION METHOD FOR C-RAF-1 GENES
12
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                                                                                                                                                                  Score 62; DB 1;
Pred. No. 3.00e+01
7; Mismatches
                                                                                                                                                                                                                                                                                         Timothy E
                                                                                                                                                                                                                                                                           ONYX-005/00US
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Query Match
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino acids
TYPE: amino acid
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US-08-185-282-1
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                           ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER:
               CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                 APPLICANT: Rapp, Ulf R.
APPLICANT: Storm, Stephen M.
TITLE OF INVENTION: DETECTION METHOD FOR C-RAF-1 GENES
                                                                                                                                                                                 ADDRESSEE:
STREET: 16
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                                                                                                                                                CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
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                                                                                                                              COUNTRY:
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APPLICATION NUMBER:
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648 AA; 72915 MW; 2223546 CN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                 E: CUSHMAN, DARBY & CUSHMAN
1615 L Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: CUSHMAN, DARBY
                                                                                                                                  USA
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US/08/185,282
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Pred. No. 3.00e+01
7; Mismatches
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                             Version
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PRIOR APPLICATION DATA:

FILING DATE: CLASSIFICATION:

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US-08-185-282-4
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08185282 Patent No. 5618670
                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Rapp, Ulf R.
APPLICANT: Storm, Stephen M.
  TELEX:
INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ANDHLSILEAWSDNDTPYLH
                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                           ZIP: 20036-5601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: WT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
VFORMATION FOR SEQ ID NO: 4:
                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: DÉTECTION METHOD FOR C-RAF-1 GENES NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE; CUSHMAN, DARBY & CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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NAME: Scott, Watson T.
                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 648 amino acids
TYPE: amino acid
TOPOLOGY: linear
NCE 648 AA; 72916 MW; 2224068 CN;
                                                   NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE/DOCKET NUMBER: WTS/5683/82732
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                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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TELEX: 6714627 CUSH
                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                    CITY:
                                                                                                                                                                                                                                                                               STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/759,738
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Pred. No. 3.00e+01
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Best Local Similarity 30.08;
                                            Query Match
Best Local
                                 Matches
                                                                                         TELEFAX: (202) 861-3000
TELEFAX: (202) 822-9944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 648 amino active the sequence of the sequence of the sequence characteristics:
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SEQUENCE 648 AA; 72856 MW; 2225122 CN;
                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08185282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION: Ulf R.
APPLICANT: Storm, Stephen M.
APPLICANT: STORM, STEPHEN M.
TITLE OF INVENTION: DETECTION
                               Local Similarity
les 6; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: DÉTECTION METHOD FOR C-RAF-1 GENES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSE: CUSHMAN, DARBY & CUSHMAN
STREET: 1515 L Street, N.W.
                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
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LENGTH: 648 amino acids
TYPE: amino acid
                                                                                                                                                                                  NAME: Scott, Watson T.
REGISTRATION NUMBER: 26,581
REFERENCE,DOCKET NUMBER: WT
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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TKDNLAIVTQWCEGSSLYKH 432
                                                                             TOPOLOGY: 11
ICE 648 AA;
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
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larity 30.0%;
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                                                                           72904 MW; 2220863 CN;
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Pred. No. 3.00e+01
                             Score 62; DB 1; Ler
Pred. No. 3.00e+01;
7; Mismatches 7;
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Search completed: Tue Jan 11 15:39:05 2000 Job time : 8 secs.